

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 24, 2005, 18:43:30 ; Search time 165 Seconds  
(without alignments)  
21.096 Million cell updates/sec

Title: US-09-914-205-5

Perfect score: 45

Sequence: 1 FVSLKIVPI 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	AAV95885	Human MHC
2	39	86.7	168	AAV99911	Peptide e
3	39	86.7	425	AAV99915	Peptide e
4	39	86.7	425	AAV99914	Peptide e
5	39	86.7	425	AAV99913	Peptide e
6	39	86.7	425	AAV99916	Peptide e
7	39	86.7	476	AAV99927	Peptide e
8	39	86.7	638	AAV99924	Peptide e
9	39	86.7	657	AAV95882	Peptide e
10	39	86.7	689	AAV99925	Peptide e
11	39	86.7	822	AAV99926	Peptide e
12	38	84.4	498	AAV37055	HIV-1 bre
13	38	84.4	498	AAW37054	HIV-1 bre
14	38	84.4	498	ADK19345	HIV DNA g
15	38	84.4	498	ADK19343	HIV DNA g
16	38	84.4	501	AAE39544	HIV gp120
17	38	84.4	501	AAE39543	HIV gp120
18	36	80.0	131	AAAG01247	Human sec
19	36	80.0	169	AAE33585	Human col
20	36	80.0	210	AAE36776	Human pro
21	36	80.0	417	ABM84029	Human dia
22	36	80.0	453	AAW54356	Ubiquinol
23	36	80.0	453	ABM04804	Human mit
24	36	80.0	453	ADG61366	Human pro
25	36	80.0	453	ADJ70409	Human hea

26	36	80.0	453	7	ADJ68715	Human hea
27	36	80.0	453	7	ADJ70408	Human hea
28	36	80.0	453	8	ABM81716	Tumour-as
29	36	80.0	468	4	AAU33278	Novel hum
30	36	80.0	469	2	AAW37061	HIV-1 bre
31	36	80.0	469	7	AAE39552	HIV gp120
32	36	80.0	469	8	ADK19359	HIV DNA g
33	35	77.8	15	2	AAW99862	HIV-1 gpl
34	35	77.8	34	2	AAW99851	HIV-1 gpl
35	35	77.8	51	3	AAH10710	HIV-1 gpl
36	35	77.8	78	5	ABP52850	HIV-1 gpl
37	35	77.8	96	2	AAW99852	HIV-1 gpl
38	35	77.8	245	6	ABP78185	N. Gonorr
39	35	77.8	245	6	ABU37576	Protein e
40	35	77.8	245	8	ADP08243	Neisseria
41	35	77.8	278	5	ABH89469	Human pol
42	35	77.8	365	2	AAW99874	Case-A2 V
43	35	77.8	453	4	AAW38830	Human pol
44	35	77.8	473	4	AAE01350	Human tum
45	35	77.8	473	4	AAW38829	Human pol

#### ALIGNMENTS

#### RESULT 1

AAV95885  
ID AAV95885 standard; peptide; 9 AA.

XX AAV95885;

XX 12-SEP-2003 (revised)

DT 20-NOV-2000 (first entry)

XX Human MHC class I allele HLA-A0201 binding motif CLP-504.

XX Major histocompatibility complex class 1; MHC class 1; human; HLA-A0201;  
KW HIV-1; human immunodeficiency virus type 1; gp140; immunogen;  
KW DNA vaccine.

XX Human immunodeficiency virus 1.

XX WO2000050604-A1.

XX 31-AUG-2000.

XX 24-FEB-2000; 2000WO-CA000190.

XX 24-FEB-1999; 99US-00256194.

XX (CONN-) CONNAUGHT LAB LTD.

XX Sia CDY, Cao S, Persson R, Rovinski B, Parrington M;

XX WPI; 2000-565457/52.

XX Vectors comprising sequences encoding the extracellular fragment of gp140  
of a primary human immunodeficiency virus (HIV)-1 isolate, useful for  
vaccinating against HIV-1.

XX Claim 18; Page 18; 37pp; English.

XX The present sequence is that of CLP-504, a major histocompatibility  
complex (MHC) class-I restricted motif of the extracellular envelope  
fragment, gp140 (see AAV95882), of HIV-1 isolate BX08. The invention  
provides vectors comprising sequences encoding gp140, useful for  
vaccinating against HIV-1. The gp140 protein is rich in motifs restricted  
to both the human and murine MHC class I alleles (see AAV95883-94). The  
present peptide is HLA-A0201 restricted. Immunisation with an immunogen  
expressing the gp140 protein leads to the generation of peptides with  
class I binding capability to allow the induction of HIV-1-specific  
cytotoxic T lymphocytes capable of killing virus-infected cells to limit  
infection. (Updated on 12-SEP-2003 to standardise OS field)

```
XX SQ - Sequence 9 AA;
Query Match      100.0%; Score 45; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
    |||||
DB 1 FYSLKIVPI 9

RESULT 2
AA999911
ID .AA999911 standard; protein; 168 AA.
XX
AC .AA999911;
XX
XX 16-NOV-2000 (first entry)
XX
XX Peptide encoded by Piece 1 DNA used in HIV DNA vaccine.
XX
XX HIV; human immunodeficiency virus; vaccine; snut;
XX silent nucleotide substitution; AIDS.
XX
XX Human immunodeficiency virus 1.
XX Synthetic.
XX
XX WO200029561-A2.
XX
XX 25-MAY-2000.
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XX 27-MAR-2000; 2000WO-DK000144.
XX
XX 29-MAR-1999; 99DK-00000427.
XX 09-APR-1999; 99US-0128558P.
XX (STAT-) STATENS SERUM INST.
XX
XX Fomsgaard A;
XX
XX WPI; 2000-387778/33.
XX N-PSDB; AAA49080.
XX
XX Producing nucleotide sequence construct with optimized codons for human
XX immunodeficiency virus (HIV) genetic vaccine involves obtaining a first
XX nucleotide sequence from a HIV patient, redesigning and assembling it
XX with snuts.
XX
XX Example 4; 108-109; 150pp; English.
XX
XX The present invention relates to a nucleotide construct with optimised
XX codons for use as a human immunodeficiency virus (HIV) DNA vaccine. The
XX construct uses codons from highly expressed mammalian proteins to code
XX for each derivative of an early, primary HIV envelope gene. The first
XX stage in the production of the construct was the cloning of an HIV
XX envelope gene. A nucleotide sequence encoding this gene was then created
XX using codons from highly expressed mammalian genes. The present sequence
XX is the protein encoded by one of the pieces (AAA49080-A49092) that were
XX made by assembly of snuts. Each derivative of the envelope gene (AAA49093
XX -A49097) was then built using the pieces. The HIV DNA vaccine may be used
XX as a prophylactic vaccine and as a therapeutic vaccine in HIV infected
XX patients
XX
XX Sequence 168 AA;
Query Match      86.7%; Score 39; DB 3; Length 168;
Best Local Similarity 88.9%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 FYSLKIVPI 9
    |||||
DB 145 FYSLDIVPI 153

RESULT 3
AA999915
ID .AA999915 standard; protein; 425 AA.
XX
AC .AA999915;
XX
XX 16-NOV-2000 (first entry)
XX
XX Peptide encoded by Piece 3GVIV2 DNA used in HIV DNA vaccine.
XX
XX HIV; human immunodeficiency virus; vaccine; snut;
XX silent nucleotide substitution; AIDS.
XX
XX Human immunodeficiency virus 1.
XX Synthetic.
XX
XX WO200029561-A2.
XX
XX 25-MAY-2000.
XX
XX 27-MAR-2000; 2000WO-DK000144.
XX
XX 29-MAR-1999; 99DK-00000427.
XX 09-APR-1999; 99US-0128558P.
XX (STAT-) STATENS SERUM INST.
XX
XX Fomsgaard A;
XX
XX WPI; 2000-387778/33.
XX N-PSDB; AAA49084.
XX
XX Producing nucleotide sequence construct with optimized codons for human
XX immunodeficiency virus (HIV) genetic vaccine involves obtaining a first
XX nucleotide sequence from a HIV patient, redesigning and assembling it
XX with snuts.
XX
XX Example 4; 117-118; 150pp; English.
XX
XX The present invention relates to a nucleotide construct with optimised
XX codons for use as a human immunodeficiency virus (HIV) DNA vaccine. The
XX construct uses codons from highly expressed mammalian proteins to code
XX for each derivative of an early, primary HIV envelope gene. The first
XX stage in the production of the construct was the cloning of an HIV
XX envelope gene. A nucleotide sequence encoding this gene was then created
XX using codons from highly expressed mammalian genes. The present sequence
XX is the protein encoded by one of the pieces (AAA49080-A49092) that were
XX made by assembly of snuts. Each derivative of the envelope gene (AAA49093
XX -A49097) was then built using the pieces. The HIV DNA vaccine may be used
XX as a prophylactic vaccine and as a therapeutic vaccine in HIV infected
XX patients
XX
XX Sequence 425 AA;
Query Match      86.7%; Score 39; DB 3; Length 425;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
    |||||
DB 145 FYSLDIVPI 153

RESULT 4
AA999914
ID .AA999914 standard; protein; 425 AA.
XX
AC .AA999914;
XX
XX 16-NOV-2000 (first entry)
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DE Peptide encoded by Piece 3GV1 DNA used in HIV DNA vaccine.  
 XX HIV; human immunodeficiency virus; vaccine; snut;  
 KW silent nucleotide substitution; AIDS.

XX Human immunodeficiency virus 1.  
 OS Synthetic.

XX WO200029561-A2.

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DE Peptide encoded by Piece 3GV1 DNA used in HIV DNA vaccine.  
 XX HIV; human immunodeficiency virus; vaccine; snut;  
 KW silent nucleotide substitution; AIDS.

XX Human immunodeficiency virus 1.  
 OS Synthetic.

XX WO200029561-A2.

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DE Peptide encoded by Piece 3GV1 DNA used in HIV DNA vaccine.  
 XX HIV; human immunodeficiency virus; vaccine; snut;  
 KW silent nucleotide substitution; AIDS.

XX Human immunodeficiency virus 1.  
 OS Synthetic.

XX WO200029561-A2.

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DE Peptide encoded by Piece 3GV1 DNA used in HIV DNA vaccine.  
 XX HIV; human immunodeficiency virus; vaccine; snut;  
 KW silent nucleotide substitution; AIDS.

XX Human immunodeficiency virus 1.  
 OS Synthetic.

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DE Peptide encoded by Piece 3GV1 DNA used in HIV DNA vaccine.  
 XX HIV; human immunodeficiency virus; vaccine; snut;  
 KW silent nucleotide substitution; AIDS.

XX Human immunodeficiency virus 1.  
 OS Synthetic.

XX WO200029561-A2.

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DE Peptide encoded by Piece 3GV1 DNA used in HIV DNA vaccine.  
 XX HIV; human immunodeficiency virus; vaccine; snut;  
 KW silent nucleotide substitution; AIDS.

XX Human immunodeficiency virus 1.  
 OS Synthetic.

XX WO200029561-A2.

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DE Peptide encoded by Piece 3GV1 DNA used in HIV DNA vaccine.  
 XX HIV; human immunodeficiency virus; vaccine; snut;  
 KW silent nucleotide substitution; AIDS.

XX Human immunodeficiency virus 1.  
 OS Synthetic.

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DE Peptide encoded by Piece 3GV1 DNA used in HIV DNA vaccine.  
 XX HIV; human immunodeficiency virus; vaccine; snut;  
 KW silent nucleotide substitution; AIDS.

XX Human immunodeficiency virus 1.  
 OS Synthetic.

XX WO200029561-A2.

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DE Peptide encoded by Piece 3GV1 DNA used in HIV DNA vaccine.  
 XX HIV; human immunodeficiency virus; vaccine; snut;  
 KW silent nucleotide substitution; AIDS.

XX Human immunodeficiency virus 1.  
 OS Synthetic.



CC A49079) were created by redesigning the nucleotide construct so that  
 CC restriction enzyme sites surrounded functional regions of the sequence.  
 CC Pieces (AAA49080-A49092) were made by assembly of the snuts. Each  
 CC derivative of the envelope gene (AAA49093-A49097) was then built using  
 CC the pieces. The present sequence is the peptide encoded by one of the  
 CC gene derivatives. The HIV DNA vaccine may be used as a prophylactic  
 CC vaccine and as a therapeutic vaccine in HIV infected patients  
 CC  
 XX  
 SQ Sequence 638 AA;

Query Match 86.7%; Score 39; DB 3; Length 638;  
 Best Local Similarity 88.9%; Pred. No. 30;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
 DB 145 FYSLDIVPI 153  
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RESULT 9  
 AAY95882  
 ID AAY95882 standard; protein; 657 AA.  
 AC AAY95882;

XX  
 XX 12-SEP-2003 (revised)  
 DT 20-NOV-2000 (first entry)  
 DT

XX HIV-1 (BX08) extracellular envelope glycoprotein gp140.

XX HIV-1; gp140; immunogen; DNA vaccine.

XX Human immunodeficiency virus 1.

XX WO2000050604-A1.

XX 31-AUG-2000.

XX 24-FEB-2000; 2000WO-CA000190.

XX 24-FEB-1999; 99US-00256194.

XX (CONN-) CONNAUGHT LAB LTD.

XX Sia CDY, Cao S, Persson R, Rovinski B, Farrington M;

XX WPI; 2000-565457/52.

XX N-PSDB; AAA50336, AAA50337.

XX Vectors comprising sequences encoding the extracellular fragment of gp140  
 of a primary human immunodeficiency virus (HIV)-1 isolate, useful for  
 PT vaccinating against HIV-1.

XX Disclosure; Fig 2A-F; 37pp; English.

XX The present sequence is that of the extracellular envelope fragment gp140  
 of HIV-1 isolate BX08. The invention relates to the design and  
 CC construction of HIV DNA-based immunogens capable of eliciting cell-  
 CC mediated immunity. The work focussed on HIV-1 BX08 gp140 because this  
 CC protein is rich in motifs restricted to both the murine and human major  
 CC histocompatibility complex class I alleles (see AAY95883-94). Vectors  
 CC such as pCMV.GP140.BX08 are provided that comprise a gp140 gene (see  
 CC AAA50336) under control of a promoter for expression of the gene product  
 CC in a host organism, thereby eliciting a cytotoxic T-cell response. The  
 CC invention also includes an immunogenic composition containing the vector  
 CC and a method for generating a cytotoxic T-cell response to HIV-1 in a  
 CC host by administering the immunogenic composition to the host. The  
 CC immunogenic compositions may be formulated for intramuscular immunisation  
 CC or gene gun delivery. (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 657 AA;

Query Match 86.7%; Score 39; DB 3; Length 657;

Best Local Similarity 88.9%; Pred. No. 31;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
 DB 162 FYSLDIVPI 170  
 |||||

RESULT 10

AAY99925

ID AAY99925 standard; protein; 689 AA.

AC AAY99925;

XX 16-NOV-2000 (first entry)

XX Peptide encoded by synBX08- 150 gene derivative used in HIV DNA vaccine.  
 KW HIV; human immunodeficiency virus; vaccine; snut;  
 KW silent nucleotide substitution; AIDS.

XX Human immunodeficiency virus 1.  
 OS Synthetic.

XX WO200029561-A2.

XX 25-MAY-2000.

XX 27-MAR-2000; 2000WO-DK000144.

XX 29-MAR-1999; 99DK-00000427.

XX 09-APR-1999; 99US-0128558P.

XX (STAT-) STATENS SERUM INST.

XX Fomsgaard A;

XX WPI; 2000-387778/33.

XX N-PSDB; AAA49094.

XX Producing nucleotide sequence construct with optimized codons for human  
 immunodeficiency virus (HIV) genetic vaccine involves obtaining a first  
 PT nucleotide sequence from a HIV patient, redesigning and assembling it  
 PT with snuts.

XX Disclosure; 137-138; 150pp; English.

XX The present invention relates to a nucleotide construct with optimised  
 CC codons for use as a human immunodeficiency virus (HIV) DNA vaccine. The  
 CC construct uses codons from highly expressed mammalian proteins to code  
 CC for each derivative of an early, primary HIV envelope gene. The first  
 CC stage in the production of the construct was the cloning of an HIV  
 CC envelope gene. A nucleotide sequence encoding this gene was then created  
 CC using codons from highly expressed mammalian genes. Snuts (AAA49060-  
 CC A49079) were created by redesigning the nucleotide construct so that  
 CC restriction enzyme sites surrounded functional regions of the sequence.  
 CC Pieces (AAA49080-A49092) were made by assembly of the snuts. Each  
 CC derivative of the envelope gene (AAA49093-A49097) was then built using  
 CC the pieces. The present sequence is the peptide encoded by one of the  
 CC gene derivatives. The HIV DNA vaccine may be used as a prophylactic  
 CC vaccine and as a therapeutic vaccine in HIV infected patients

XX Sequence 689 AA;

Query Match 86.7%; Score 39; DB 3; Length 689;

Best Local Similarity 88.9%; Pred. No. 32;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
 DB 145 FYSLDIVPI 153  
 |||||

## RESULT 11

AAV99926  
 ID AAV99926 standard; protein; 822 AA.  
 XX  
 AC AAV99926;  
 XX  
 DT 16-NOV-2000 (first entry)  
 XX  
 DE Peptide encoded by synBX08- 160 gene derivative used in HIV DNA vaccine.  
 XX  
 KW HIV; human immunodeficiency virus; vaccine; snut;  
 KW silent nucleotide substitution; AIDS.  
 XX  
 OS Synthetic.  
 OS  
 FN WO200029561-A2.  
 XX  
 XX 25-MAY-2000.  
 PD  
 XX 27-MAR-2000; 2000WO-DK000144.  
 PF  
 XX 29-MAR-1999; 99DK-00000427.  
 PR  
 PR 09-APR-1999; 99US-0128558P.  
 XX  
 PA (STAT-) STATENS SERUM INST.  
 XX  
 PI Fomsgaard A;  
 PI  
 XX WPI; 2000-387778/33.  
 DR  
 DR N-PSDB; AAA49095.  
 XX

XX Producing nucleotide sequence construct with optimized codons for human immunodeficiency virus (HIV) genetic vaccine involves obtaining a first nucleotide sequence from a HIV patient, redesigning and assembling it with snuts.

XX Disclosure; 142-144; 150pp; English.

XX The present invention relates to a nucleotide construct with optimised codons for use as a human immunodeficiency virus (HIV) DNA vaccine. The construct uses codons from highly expressed mammalian proteins to code for each derivative of an early, primary HIV envelope gene. The first stage in the production of the construct was the cloning of an HIV envelope gene. A nucleotide sequence encoding this gene was then created using codons from highly expressed mammalian genes. Snuts (AAA49060-A49079) were created by redesigning the nucleotide construct so that restriction enzyme sites surrounded functional regions of the sequence. Pieces (AAA49080-A49092) were made by assembly of the snuts. Each derivative of the envelope gene (AAA49093-A49097) was then built using the pieces. The present sequence is the peptide encoded by one of the gene derivatives. The HIV DNA vaccine may be used as a prophylactic vaccine and as a therapeutic vaccine in HIV infected patients

XX Sequence 822 AA;

Query Match 86.7%; Score 39; DB 3; Length 822;  
 Best Local Similarity 88.9%; Pred. No. 39;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
 DB 145 FYSLDIVPI 153

## RESULT 12

AAW37055  
 ID AAW37055 standard; protein; 498 AA.  
 XX  
 AC AAW37055;  
 XX  
 DT 17-OCT-2003 (revised)  
 DT 20-JUL-1998 (first entry)

XX HIV-1 breakthrough isolate clone C6.5 gp120 polypeptide.  
 XX  
 KW HIV-1; envelope protein; gp120; MN-rgp120; vaccine; AIDS.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 67  
 FT /note= "encoded by ANT"

PN WO9801564-A1.

XX 15-JAN-1998.

XX 03-JUL-1997; 97WO-US009690.

XX 08-JUL-1996; 96US-0676737P.

XX (GETH ) GENENTECH INC.

XX Berman PW;

XX WPI; 1998-101059/09.

XX N-PSDB; AAV00518.

XX Human immunodeficiency virus gp120 sequences from vaccine breakthrough strains - useful in providing added protection against HIV not provided by original vaccine.

XX Claim 1; Page 95-98; 193pp; English.

XX This is the deduced sequence of a gp120 envelope polypeptide of clone C6.5 of a HIV-1 breakthrough isolate obtained from an individual infected with HIV-1 through high risk activity while participating in Phase I or Phase 2 trials of MN-rgp120, a candidate recombinant gp120 HIV-1 vaccine. Nucleotide sequences (see AAV00517-30) for gp120 polypeptides (see AAW37054-67) were obtained from 2 clones of each of 7 breakthrough isolates. All 7 envelope glycoproteins have sequences typical of subtype (clade) B viruses. The overall homology with MN-rgp120 is 69-80%. Use of the gp120 polypeptides from one or more of the breakthrough isolates, usually together with MN-rgp120, can provide protection against HIV strains that are sufficiently different from the vaccine strain (e.g. MN-rgp120) that the vaccine does not confer protection against those strains. The gp120 proteins can also be used in screening assays to identify antagonists of CC-CKR chemokine receptors. Antibodies induced by the polypeptides are also provided. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 498 AA;

Query Match 84.4%; Score 38; DB 2; Length 498;  
 Best Local Similarity 77.8%; Pred. No. 37;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
 DB 156 FYSLDWPI 164

## RESULT 13

AAW37054  
 ID AAW37054 standard; protein; 498 AA.

XX AAW37054;

XX 17-OCT-2003 (revised)

DT 20-JUL-1998 (first entry)

DE HIV-1 breakthrough isolate clone C6.1 gp120 polypeptide.

XX HIV-1; envelope protein; gp120; MN-rgp120; vaccine; AIDS.

XX

OS Human immunodeficiency virus 1.  
 XX WO9801564-A1.  
 PN  
 XX  
 PD 15-JAN-1998.  
 XX  
 XX 03-JUL-1997; 97WO-US009690.  
 PF  
 XX  
 PR 08-JUL-1996; 96US-0676737P.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 PI Berman PW;  
 XX  
 XX WPI: 1998-101059/09.  
 DR N-PSDB; AAV00517.  
 DR  
 XX  
 PT Human immunodeficiency virus gp120 sequences from vaccine breakthrough  
 PT strains - useful in providing added protection against HIV not provided  
 PT by original vaccine.  
 PT  
 PS Claim 1; Page 91-94; 193pp; English.  
 XX  
 CC This is the deduced sequence of a gp120 envelope polypeptide of clone  
 CC C6.1 of a HIV-1 breakthrough isolate obtained from an individual infected  
 CC with HIV-1 through high risk activity while participating in Phase I or  
 CC Phase 2 trials of MN-rgp120, a candidate recombinant gp120 HIV-1 vaccine.  
 CC Nucleotide sequences (see AAV00517-30) for gp120 polypeptides (see  
 CC AAV37054-67) were obtained from 2 clones of each of 7 breakthrough  
 CC isolates. All 7 envelope glycoproteins have sequences typical of subtype  
 CC (clade) B viruses. The overall homology with MN-rgp120 is 69-80%. Use of  
 CC the gp120 polypeptides from one or more of the breakthrough isolates,  
 CC usually together with MN-rgp120, can provide protection against HIV  
 CC strains that are sufficiently different from the vaccine strain (e.g. MN-  
 CC rgp120) that the vaccine does not confer protection against those  
 CC strains. The gp120 proteins can also be used in screening assays to  
 CC identify antagonists of CC-CKR chemokine receptors. Antibodies induced by  
 CC the polypeptides are also provided. (Updated on 17-OCT-2003 to  
 CC standardise OS field)  
 XX  
 SQ Sequence 498 AA;  
 Query Match 84.4%; Score 38; DB 2; Length 498;  
 Best Local Similarity 77.8%; Pred. No. 37;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 FYSLKIVPI 9  
 Db 156 FYSLDVPPI 164  
 RESULT 14  
 ADK19345  
 ID ADK19345 standard; protein; 498 AA.  
 XX  
 AC ADK19345;  
 XX  
 DT 03-JUN-2004 (first entry)  
 DE  
 DE HIV DNA gp120 clone C6.5.  
 XX  
 KW HIV; gp120; envelope glycoprotein; AIDS; vaccine; breakthrough isolate;  
 KW gp120 MN; gp120 A244; gp120 MN-GNE8; gp120 MN-GNE8; recombinant gp120;  
 KW HIV infection.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 XX US2004052821-A1.  
 PN  
 XX 18-MAR-2004.  
 PD  
 XX 21-FEB-2003; 2003US-00371472.  
 PF  
 XX  
 XX

PR 08-JUL-1996; 96US-0069891P.  
 PR 08-JUL-1997; 97US-00889841.  
 PR 15-OCT-1999; 99US-00419362.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 PI Berman PW;  
 XX  
 XX WPI: 2004-247705/23.  
 DR N-PSDB; ADK19344.  
 DR  
 XX  
 PT New isolated human immunodeficiency virus envelope polypeptides and  
 PT oligonucleotides encoding the gp120 glycoproteins, useful for diagnosing,  
 PT preventing or treating human immunodeficiency virus (HIV) infection.  
 XX  
 PS Claim 6; SEQ ID NO 5; 126pp; English.  
 XX  
 CC The invention relates to an isolated polypeptide comprising an HIV (human  
 CC immunodeficiency virus) gp120 (envelope glycoprotein 120) amino acid  
 CC sequence and its fragment from a breakthrough isolate HIV strain isolated  
 CC from a vaccinee vaccinated with the first HIV gp120 polypeptide sequence  
 CC comprises gp120 MN, gp120 A244, gp120 MN-GNE6 or gp120 MN-GNE8  
 CC (recombinant gp120). Also included are an oligonucleotide of not more  
 CC than 5 kilobases encoding the HIV gp120 polypeptide sequence, a vaccine  
 CC comprising gp120 MN and the HIV gp120 polypeptide sequence (or fragment)  
 CC in a suitable carrier and preparing an HIV vaccine (comprising adding an  
 CC HIV gp120 polypeptide sequence or its fragments from a breakthrough  
 CC isolate from a vaccinee to the vaccine with which the vaccinee was  
 CC vaccinated). The composition and methods are useful for diagnosing,  
 CC preventing or treating HIV infection (AIDS). NOTE: The authors have mixed  
 CC up the SEQ ID numbers between the sequence listing and the  
 CC description/claims, subsequently some sequences are claimed which may not  
 CC have been intended to be claimed and some sequences which were intended  
 CC to be claimed are not claimed, other sequences cannot be identified from  
 CC the information given in the patent. The present sequence represents a  
 CC gp120 protein from a breakthrough isolate HIV strain.  
 XX  
 SQ Sequence 498 AA;  
 Query Match 84.4%; Score 38; DB 8; Length 498;  
 Best Local Similarity 77.8%; Pred. No. 37;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 FYSLKIVPI 9  
 Db 156 FYSLDVPPI 164  
 RESULT 15  
 ADK19343  
 ID ADK19343 standard; protein; 498 AA.  
 XX  
 AC ADK19343;  
 XX  
 DT 03-JUN-2004 (first entry)  
 DE  
 DE HIV DNA gp120 clone C6.1.  
 XX  
 KW HIV; gp120; envelope glycoprotein; AIDS; vaccine; breakthrough isolate;  
 KW gp120 MN; gp120 A244; gp120 MN-GNE6; gp120 MN-GNE8; recombinant gp120;  
 KW HIV infection.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 XX US2004052821-A1.  
 PN  
 XX 18-MAR-2004.  
 PD  
 XX 21-FEB-2003; 2003US-00371472.  
 PF  
 XX  
 XX 08-JUL-1996; 96US-0069891P.  
 PR 08-JUL-1997; 97US-00889841.  
 PR 15-OCT-1999; 99US-00419362.  
 PR

```

XX (GETH ) GENENTECH INC.
XX Berman PW;
XX WPI; 2004-247705/23.
XX N-PSDB; ADK19342.
XX
XX New isolated human immunodeficiency virus envelope polypeptides and
XX oligonucleotides encoding the gp120 glycoproteins, useful for diagnosing,
XX preventing or treating human immunodeficiency virus (HIV) infection.
XX
XX Claim 1; SEQ ID NO 2; 126pp; English.
XX
XX The invention relates to an isolated polypeptide comprising an HIV (human
XX immunodeficiency virus) gp120 (envelope glycoprotein 120) amino acid
XX sequence and its fragment from a breakthrough isolate HIV strain isolated
XX from a vaccinee vaccinated with the first HIV gp120 polypeptide sequence
XX comprises gp120 MN, gp120 A244, gp120 MN-GNE6 or gp120 MN-GNE8
XX (recombinant gp120). Also included are an oligonucleotide of not more
XX than 5 kilobases encoding the HIV gp120 polypeptide sequence, a vaccine
XX comprising gp120 MN and the HIV gp120 polypeptide sequence (or fragment)
XX in a suitable carrier and preparing an HIV vaccine (comprising adding an
XX HIV gp120 polypeptide sequence or its fragments from a breakthrough
XX isolate from a vaccinee to the vaccine with which the vaccinee was
XX vaccinated). The composition and methods are useful for diagnosing,
XX preventing or treating HIV infection (AIDS). NOTE: The authors have mixed
XX up the SEQ ID numbers between the sequence listing and the
XX description/claims, subsequently some sequences are claimed which may not
XX have been intended to be claimed and some sequences which were intended
XX to be claimed are not claimed, other sequences cannot be identified from
XX the information given in the patent. The present sequence represents a
XX gp120 protein from a breakthrough isolate HIV strain.
XX
XX Sequence 498 AA;
SQ
Query Match 84.4%; Score 38; DB 8; Length 498;
Best Local Similarity 77.8%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
Db 156 FVSLDVVPI 164

RESULT 16
AAE39544
ID AAE39544 standard; protein; 501 AA.
XX
XX AAE39544;
AC
XX
XX 18-DEC-2003 (first entry)
XX
XX HIV gp120 protein from C6.5 clone.
XX
XX Envelope glycoprotein; gp120 protein; human immunodeficiency virus; HIV;
XX immunogenic; vaccine.
XX
XX Human immunodeficiency virus.
XX
XX Key Location/Qualifiers
XX Region 2..90
XX Misc-difference 67
XX /note= "Conserved region 1"
XX /note= "Encoded by ANT"
XX Region 91..136
XX /note= "variable region 1"
XX Region 137..176
XX /note= "variable region 2"
XX Region 177..275
XX /note= "Conserved region 2"
XX Region 276..310
XX /note= "variable region 3"
XX

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FT Region 311..356
FT /note= "Conserved region 3"
FT Region 363..416
FT /note= "Conserved region 4 and variable region 4"
FT Region 430..441
FT /note= "Variable region 5"
FT Region 442..484
FT /note= "Conserved region 5"
FT Misc-difference 499..501
FT /note= "These residues are absent in the sequence shown
FT as SEQ ID NO: 5 in column 83-86 of the specification"
FT Misc-difference 499
FT /note= "Encoded by TAA; This residue is absent in the
FT sequence shown in column 79-83 of the specification"
XX
XX US6585979-B1.
XX
XX 01-JUL-2003.
XX
XX 15-OCT-1999; 99US-00419362.
XX
XX 08-JUL-1997; 97US-00889841.
XX 17-DEC-1997; 97US-0069891P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Berman PW;
XX
XX WPI; 2003-707284/67.
XX N-PSDB; AAD60060.
XX
XX An immunogenic composition, useful as a vaccine against HIV, comprises a
XX polypeptide having a gp120 MN sequence and a polypeptide having a
XX breakthrough isolate gp120, in a carrier.
XX
XX Claim 1; Col 9-13; 117pp; English.
XX
XX The present invention relates to envelope glycoproteins (gp120) proteins
XX from breakthrough isolates of human immunodeficiency virus (HIV) trials.
XX The invention also relates to an immunogenic composition comprising a
XX gp120 MN sequence and a polypeptide having a breakthrough isolate gp120,
XX in a carrier. The composition is useful as a vaccine against HIV. The
XX present sequence is HIV gp120 protein
XX
XX Sequence 501 AA;
SQ
Query Match 84.4%; Score 38; DB 7; Length 501;
Best Local Similarity 77.8%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
Db 156 FVSLDVVPI 164

RESULT 17
AAE39543
ID AAE39543 standard; protein; 501 AA.
XX
XX AAE39543;
AC
XX
XX 18-DEC-2003 (first entry)
XX
XX HIV gp120 protein from C6.1 clone.
XX
XX Envelope glycoprotein; gp120 protein; human immunodeficiency virus; HIV;
XX immunogenic; vaccine.
XX
XX Human immunodeficiency virus.
XX
XX Key Location/Qualifiers
XX Region 2..90
XX /note= "Conserved region 1"
XX

```



FT Region 91. .136  
FT /note= "Variable region 1"  
FT Region 137. .176  
FT /note= "Variable region 2"  
FT Region 177. .275  
FT /note= "Conserved region 2"  
FT Region 276. .310  
FT /note= "Variable region 3"  
FT Region 311. .356  
FT /note= "Conserved region 3"  
FT Region 363. .416  
FT /note= "Conserved region 4 and variable region 4"  
FT Region 430. .441  
FT /note= "Variable region 5"  
FT Region 442. .484  
FT /note= "Conserved region 5"  
FT Misc-difference 499. .501  
FT /note= "These residues are absent in the sequence shown  
FT as SEQ ID NO: 2 in column 75-80 of the specification"  
FT Misc-difference 499  
FT /note= "Encoded by TAA; This residue is absent in the  
FT sequence shown in column 73-76 of the specification"  
XX  
PN US6585979-B1.  
XX  
XX 01-JUL-2003.  
XX  
XX 15-OCT-1999; 99US-00419362.  
XX  
XX 08-JUL-1997; 97US-00889841.  
PR 17-DEC-1997; 97US-0069891P.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Berman PW;  
XX  
XX WPI; 2003-707284/67.  
DR N-PSDB; AAD60059.  
XX  
XX An immunogenic composition, useful as a vaccine against HIV, comprises a  
FT polypeptide having a gp120 MN sequence and a polypeptide having a  
FT breakthrough isolate gp120, in a carrier.  
XX  
XX Claim 1; Col 8-9; 117pp; English.  
XX  
XX The present invention relates to envelope glycoproteins (gp120) proteins  
CC from breakthrough isolates of human immunodeficiency virus (HIV) trials.  
CC The invention also relates to an immunogenic composition comprising a  
CC gp120 MN sequence and a polypeptide having a breakthrough isolate gp120,  
CC in a carrier. The composition is useful as a vaccine against HIV. The  
CC present sequence is HIV gp120 protein  
XX  
SQ Sequence 501 AA;  
Query Match 84.4%; Score 38; DB 7; Length 501;  
Best Local Similarity 77.8%; Pred. No. 37;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FYSLKIVPI 9  
DB 156 FYSLDVWPI 164  
RESULT 18  
AAG01247  
ID AAG01247 standard; protein; 131 AA.  
XX  
AC AAG01247;  
XX  
XX 06-OCT-2000 (first entry)  
DT  
XX Human secreted protein, SEQ ID NO: 5328.  
DE  
XX

KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
KW gene therapy; chromosome mapping.  
XX  
OS Homo sapiens.  
XX  
PN EP1033401-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 21-FEB-2000; 2000EP-00200610.  
XX  
PR 26-FEB-1999; 99US-0122487P.  
XX  
PA (GEST ) GENSET.  
XX  
PI Dumas Milne Edwards J, Duclert A, Giordano J;  
XX  
XX WPI; 2000-500381/45.  
DR N-PSDB; AAC01253.  
XX  
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
FT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
FT diagnostic, forensic, gene therapy and chromosome mapping procedures.  
XX  
PS Claim 13; SEQ ID NO 5328; 71pp + Sequence Listing; English.  
XX  
XX The present sequence is a polypeptide encoded by one of a large number of  
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were  
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different  
CC tissues. EST sequences usually correspond mainly to the 3' untranslated  
CC region (UTR) of the mRNA because they are often obtained from oligo-dT  
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA  
CC sequences derived from the 5' ends of mRNAs and even in those cases where  
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely  
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can  
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs  
CC are also used in diagnostic, forensic, gene therapy and chromosome  
CC mapping procedures. They are used to obtain upstream regulatory sequences  
CC and to design expression and secretion vectors  
XX  
SQ Sequence 131 AA;  
Query Match 80.0%; Score 36; DB 3; Length 131;  
Best Local Similarity 75.0%; Pred. No. 23;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FYSLKIVP 8  
DB 13 FYSLKVAP 20  
RESULT 19  
AAB53585  
ID AAB53585 standard; protein; 169 AA.  
XX  
AC AAB53585;  
XX  
XX 09-MAR-2001 (first entry)  
DT  
XX Human colon cancer antigen protein sequence SEQ ID NO:1125.  
DE  
XX Human; colon cancer; colon cancer antigen; diagnosis; detection;  
KW identification; cytostatic; cardioactive; neuroprotective; vulnery;  
KW immunomodulatory; muscular; gynaecological; gastrointestinal;  
KW nephrotropic; antifective; antibacterial; gene therapy; wound;  
KW neural disorder; immune system disorder; muscular disorder;  
KW reproductive disorder; gastrointestinal disorder; renal disorder;  
KW infectious disease; cardiovascular disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200055351-A1.  
XX

```
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US005883.
XX
PR 12-MAR-1999; 99US-0124270P.
XX
PA (HUMA-)-HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-587534/55.
DR N-PSDB; AAC98342.
XX
PT Colon cancer associated gene sequences, referred to as colon cancer
PT antigens, useful for the treatment, prevention, and diagnosis of colon
PT disorders such as colon cancer.
XX
PS Claim 11; Page 1715; 2104pp; English.
XX
CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
CC vulnery, nephrotropic, antiinfective and antibacterial activities, and
CC can be used in gene therapy. The colon cancer antigen polynucleotides,
CC proteins and antibodies to the proteins are useful for the prevention,
CC treatment and diagnosis of colon disorders, such as colon cancer. The
CC polynucleotides may be used in diagnostics and research, such as for
CC chromosome identification, and as hybridisation probes. The proteins may
CC also be used to prevent diseases such as neural disorders, immune system
CC disorders, muscular disorders, reproductive disorders, gastrointestinal
CC disorders, wounds, renal disorders, infectious diseases, and
CC cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 169 AA;
Query Match 80.0%; Score 36; DB 3; Length 169;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 FVSLKIVP 8
DB 14 FVSLKVAP 21
RESULT 20
AAB56776
ID AAB56776 standard; protein; 210 AA.
XX
AC AAB56776;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human prostate cancer antigen protein sequence SEQ ID NO:1354.
XX
KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW vulnery; gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease.
XX
OS Homo sapiens.
XX
PN WO2000055174-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US005988.
XX
PR 12-MAR-1999; 99US-0124270P.
XX
PA (HUMA-)-HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-587534/55.
DR N-PSDB; AAC98342.
XX
PT Colon cancer associated gene sequences, referred to as colon cancer
PT antigens, useful for the treatment, prevention, and diagnosis of colon
PT disorders such as colon cancer.
XX
PS Claim 11; Page 1715; 2104pp; English.
XX
CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
CC vulnery, nephrotropic, antiinfective and antibacterial activities, and
CC can be used in gene therapy. The colon cancer antigen polynucleotides,
CC proteins and antibodies to the proteins are useful for the prevention,
CC treatment and diagnosis of colon disorders, such as colon cancer. The
CC polynucleotides may be used in diagnostics and research, such as for
CC chromosome identification, and as hybridisation probes. The proteins may
CC also be used to prevent diseases such as neural disorders, immune system
CC disorders, muscular disorders, reproductive disorders, gastrointestinal
CC disorders, wounds, renal disorders, infectious diseases, and
CC cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 169 AA;
Query Match 80.0%; Score 36; DB 3; Length 169;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 FVSLKIVP 8
DB 14 FVSLKVAP 21
RESULT 20
AAB56776
ID AAB56776 standard; protein; 210 AA.
XX
AC AAB56776;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human prostate cancer antigen protein sequence SEQ ID NO:1354.
XX
KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW vulnery; gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease.
XX
OS Homo sapiens.
XX
PN WO2000055174-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US005988.
XX
PR 12-MAR-1999; 99US-0124270P.
XX
PA (HUMA-)-HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-587534/55.
DR N-PSDB; AAC98342.
XX
PT Colon cancer associated gene sequences, referred to as prostate cancer
PT antigens, useful for treatment, prevention, and diagnosis of disorders
PT such as prostate cancer.
XX
PS Claim 11; Page 1779-1780; 2338pp; English.
XX
CC AAF15566 to AAF16505 encode the human prostate cancer associated
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
CC The prostate cancer antigens can have neuroprotective, cytostatic,
CC cardioactive, immunomodulatory, muscular, vulnery, gastrointestinal,
CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC AAB57303 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 210 AA;
Query Match 80.0%; Score 36; DB 3; Length 210;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 FVSLKIVP 8
DB 14 FVSLKVAP 21
RESULT 21
AABM84029
ID AABM84029 standard; protein; 417 AA.
XX
AC AABM84029;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4278.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Deleane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SE, Rioux P, Shen EU, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
```

XX WPI; 2004-329368/30.  
DR N-PSDB; ACN42681.  
XX  
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful  
PT in diagnosing a condition, disease or disorder associated with human  
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
PT in gene mapping.  
XX  
PS Claim 27; Page; 190pp; English.  
XX  
XX The invention relates to novel diagnostic and therapeutic polynucleotides  
CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated  
CC with human molecules, e.g. cell proliferative disorders,  
CC autoimmune/inflammatory disorders, gastrointestinal disorders, endocrine  
CC disorder, neurological disorders, developmental disorders, or  
CC infections caused by virus, bacteria, fungi or parasite. The dithp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germline  
CC gene therapy. The present sequence represents a dithp protein of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)  
XX  
SQ Sequence 417 AA;  
Query Match 80.0%; Score 36; DB 8; Length 417;  
Best Local Similarity 75.0%; Pred. No. 80;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FYSLKIVP 8  
DB 13 FYSLKVP 20  
|||||:|  
RESULT 22  
AAW54356  
ID AAW54356 standard; protein; 453 AA.  
XX  
AC AAW54356;  
XX  
DT 14-AUG-1998 (first entry)  
XX  
DE Ubiquinolcytochrom C reductase complex core protein 2 precursor.  
XX  
KW Endometrium; hyperplasia; adenocarcinoma; proliferative phase;  
KW 2D gel electrophoresis; detection.  
XX  
OS Homo sapiens.  
XX  
PN WO9810291-A1.  
XX  
PD 12-MAR-1998.  
XX  
PF 05-SEP-1997; 97WO-GB002394.  
XX  
PR 06-SEP-1996; 96GB-00018600.  
PR 08-APR-1997; 97GB-00007132.  
XX  
XX (CLIN-) CENT CLINICAL & BASIC RES.  
XX  
XX Byrjalsen I, Larsen P, Fey SJ;  
PI WPI; 1998-207057/18.  
DR  
XX Biochemical markers of human endometrium - useful for, e.g. diagnosis of  
PT hyperplasia and adenocarcinoma.  
XX  
PS Disclosure; Page 21; 77pp; English.

XX Proteins AAW54349-W54364 are examples of proteins produced in the  
CC endometrium during the hyperplasia, adenocarcinoma or proliferative phase  
CC of the endometrium. The presence and quantities of these proteins can be  
CC detected using 2D gel electrophoresis comparison of cell lysates. The  
CC proteins can be used as biochemical markers to detect the phase of the  
CC endometrium and can be measured in body fluids, obviating the need for  
CC endometrial biopsies  
XX  
SQ Sequence 453 AA;  
Query Match 80.0%; Score 36; DB 2; Length 453;  
Best Local Similarity 75.0%; Pred. No. 87;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FYSLKIVP 8  
DB 13 FYSLKVP 20  
|||||:|  
RESULT 23  
ABM04804  
ID ABM04804 standard; protein; 453 AA.  
XX  
AC ABM04804;  
XX  
DT 22-SEP-2003 (first entry)  
XX  
DE Human mitochondrial cytochrome bc-1 complex core protein II.  
XX  
KW spinal cord; neuropathic pain; central sensitisation pain; pain;  
KW analgesic; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN EP1284298-A2.  
XX  
PD 19-FEB-2003.  
XX  
PF 26-JUL-2002; 2002EP-00255229.  
XX  
PR 27-JUL-2001; 2001GB-00018354.  
PR 07-FEB-2002; 2002GB-00002883.  
XX  
XX (WARN ) WARNER LAMBERT CO.  
XX  
PI Brooksbank RA, Dixon AK, Lee K, Pinnock RD;  
XX  
DR WPI; 2003-543489/52.  
DR N-PSDB; ACF25346.  
XX  
PT Use of an isolated gene sequence in the screening of compounds for  
PT diagnosing or treating pain.  
XX  
PS Claim 1; Page 85-86; 188pp; English.  
XX  
XX The invention relates to a novel isolated gene sequence that is  
CC downregulated in the spinal cord of a mammal in response to mechanically  
CC distinct first and second models of neuropathic or central sensitisation  
CC pain, useful in the screening of compounds for diagnosing or treating  
CC pain. A protein encoded by a gene of the invention has analgesic  
CC activity. A polynucleotide of the invention may have a use in gene  
CC therapy. The gene sequence is useful for preparing a composition for  
CC diagnosing or treating pain. The present sequence represents a protein  
CC encoded by a gene of the invention  
XX  
SQ Sequence 453 AA;  
Query Match 80.0%; Score 36; DB 6; Length 453;  
Best Local Similarity 75.0%; Pred. No. 87;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 FYSLKIVP 8

|||||: |  
13 FYSLKVP 20

Db

RESULT 24  
ADE61366  
ID ADE61366 standard; protein; 453 AA.  
XX  
AC ADE61366;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human Protein P22695, SEQ ID NO 7284.  
XX  
KW Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
OS Homo sapiens.  
XX  
PN WO2003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX  
DR WPI; 2003-268312/26.  
DR GENBANK; P22695.  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
PS Claim 1; Page; 1017pp; English.  
XX  
CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 453 AA;

Query Match 80.0%; Score 36; DB 7; Length 453;  
Best Local Similarity 75.0%; Pred. No. 87;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 FYSLKVP 8  
|||: |  
Db 13 FYSLKVP 20

RESULT 25  
ADJ70409  
ID ADJ70409 standard; protein; 453 AA.  
XX  
AC ADJ70409;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human heat mitochondrial protein as a therapeutic target SeqID2215.  
XX  
KW mitochondrial; human; screening assay; diabetes mellitus;  
KW Huntington's disease; osteoarthritis;  
KW Leber's hereditary optic neuropathy; LHON;  
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;  
KW osteopathic; ophthalmological; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO2003087768-A2.  
XX  
PD 23-OCT-2003.  
XX  
PF 04-APR-2003; 2003WO-US010870.  
XX  
PR 12-APR-2002; 2002US-0372843P.  
PR 17-JUN-2002; 2002US-0399987P.  
PR 20-SEP-2002; 2002US-0412418P.  
XX  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
XX  
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;  
PI Warnock DE;  
XX  
DR WPI; 2003-845369/78.  
XX  
PT Identifying a mitochondrial target for drug screening assays and for  
PT treating diseases associated with altered mitochondrial function,  
PT comprises detecting a modified polypeptide in a sample and correlating  
PT with the disease.  
XX  
PS Claim 1; SEQ ID NO 2215; 180pp; English.  
XX  
CC This invention relates to novel mitochondrial targets that can be used  
CC for therapeutic intervention in treating a disease associated with  
CC altered mitochondrial function. Specifically, it refers to a method for  
CC identifying proteins of the human heart mitochondrial proteome that are  
CC useful for drug screening assays, as well as therapeutic targets. The  
CC present invention describes a method for identifying such proteins that  
CC can be used in the treatment of various diseases associated with altered  
CC mitochondrial function including diabetes mellitus, Huntington's disease,  
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
CC compositions have neuroprotective, nootropic, antidiabetic,  
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
CC cytostatic activities. This polypeptide sequence is a human heart  
CC mitochondrial protein of the invention.  
XX  
SQ Sequence 453 AA;

Query Match 80.0%; Score 36; DB 7; Length 453;

Best Local Similarity 75.0%; Pred. No. 87;		Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
OY	1 FYSLKIVP 8	Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
Db	13 FYSLKVP 20		
RESULT 26			
ADJ68715	ADJ68715 standard; protein; 453 AA.		
XX	AC	ADJ68715;	
XX	DT	06-MAY-2004 (first entry)	
XX	DE	Human heat mitochondrial protein as a therapeutic target SeqID521.	
XX	KW	mitochondrial; human; screening assay; diabetes mellitus;	
XX	KW	Huntington's disease; osteoarthritis;	
XX	KW	Leber's hereditary optic neuropathy; LHON;	
XX	KW	mitochondrial encephalopathy lactic acidosis and stroke; MELAS;	
XX	KW	myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;	
XX	KW	neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;	
XX	KW	osteopathic; ophthalmological; cytostatic.	
XX	OS	Homo sapiens.	
XX	PN	WO2003087768-A2.	
XX	PD	23-OCT-2003.	
XX	PF	04-APR-2003; 2003WO-US010870.	
XX	PR	12-APR-2002; 2002US-0372843P.	
XX	PR	17-JUN-2002; 2002US-0389987P.	
XX	PR	20-SEP-2002; 2002US-0412418P.	
XX	PA	(MITO-) MITOKOR.	
XX	PA	(BUCK-) BUCK INST AGE RES.	
XX	PI	Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;	
XX	PI	Warnock DE;	
XX	XX	WPI; 2003-845369/78.	
XX	XX	Identifying a mitochondrial target for drug screening assays and for	
XX	PT	treating diseases associated with altered mitochondrial function,	
XX	PT	comprises detecting a modified polypeptide in a sample and correlating	
XX	PT	with the disease.	
XX	PS	Claim 1; SEQ ID NO 521; 180pp; English.	
XX	CC	This invention relates to novel mitochondrial targets that can be used	
XX	CC	for therapeutic intervention in treating a disease associated with	
XX	CC	altered mitochondrial function. Specifically, it refers to a method for	
XX	CC	identifying proteins of the human heart mitochondrial proteome that are	
XX	CC	useful for drug screening assays, as well as therapeutic targets. The	
XX	CC	present invention describes a method for identifying such proteins that	
XX	CC	can be used in the treatment of various diseases associated with altered	
XX	CC	mitochondrial function including diabetes mellitus, Huntington's disease,	
XX	CC	osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial	
XX	CC	encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy	
XX	CC	ragged red fibre syndrome (MERRF) or cancer. Accordingly, these	
XX	CC	compositions have neuroprotective, nootropic, antidiabetic,	
XX	CC	anticonvulsant, antiarthritic, osteopathic, ophthalmological and	
XX	CC	cytostatic activities. This polypeptide sequence is a human heart	
XX	CC	mitochondrial protein of the invention.	
XX	SQ	Sequence 453 AA;	
Query Match		80.0%; Score 36; DB 7; Length 453;	
Best Local Similarity		75.0%; Pred. No. 87;	
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			

Best Local Similarity 75.0%; Pred. No. 87;		Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
OY	1 FYSLKIVP 8	Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
Db	13 FYSLKVP 20		
RESULT 27			
ADJ70408	ADJ70408 standard; protein; 453 AA.		
XX	AC	ADJ70408;	
XX	DT	06-MAY-2004 (first entry)	
XX	DE	Human heat mitochondrial protein as a therapeutic target SeqID2214.	
XX	KW	mitochondrial; human; screening assay; diabetes mellitus;	
XX	KW	Huntington's disease; osteoarthritis;	
XX	KW	Leber's hereditary optic neuropathy; LHON;	
XX	KW	mitochondrial encephalopathy lactic acidosis and stroke; MELAS;	
XX	KW	myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;	
XX	KW	neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;	
XX	KW	osteopathic; ophthalmological; cytostatic.	
XX	OS	Homo sapiens.	
XX	PN	WO2003087768-A2.	
XX	PD	23-OCT-2003.	
XX	PF	04-APR-2003; 2003WO-US010870.	
XX	PR	12-APR-2002; 2002US-0372843P.	
XX	PR	17-JUN-2002; 2002US-0389987P.	
XX	PR	20-SEP-2002; 2002US-0412418P.	
XX	PA	(MITO-) MITOKOR.	
XX	PA	(BUCK-) BUCK INST AGE RES.	
XX	PI	Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;	
XX	PI	Warnock DE;	
XX	XX	WPI; 2003-845369/78.	
XX	XX	Identifying a mitochondrial target for drug screening assays and for	
XX	PT	treating diseases associated with altered mitochondrial function,	
XX	PT	comprises detecting a modified polypeptide in a sample and correlating	
XX	PT	with the disease.	
XX	PS	Claim 1; SEQ ID NO 2214; 180pp; English.	
XX	CC	This invention relates to novel mitochondrial targets that can be used	
XX	CC	for therapeutic intervention in treating a disease associated with	
XX	CC	altered mitochondrial function. Specifically, it refers to a method for	
XX	CC	identifying proteins of the human heart mitochondrial proteome that are	
XX	CC	useful for drug screening assays, as well as therapeutic targets. The	
XX	CC	present invention describes a method for identifying such proteins that	
XX	CC	can be used in the treatment of various diseases associated with altered	
XX	CC	mitochondrial function including diabetes mellitus, Huntington's disease,	
XX	CC	osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial	
XX	CC	encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy	
XX	CC	ragged red fibre syndrome (MERRF) or cancer. Accordingly, these	
XX	CC	compositions have neuroprotective, nootropic, antidiabetic,	
XX	CC	anticonvulsant, antiarthritic, osteopathic, ophthalmological and	
XX	CC	cytostatic activities. This polypeptide sequence is a human heart	
XX	CC	mitochondrial protein of the invention.	
XX	SQ	Sequence 453 AA;	
Query Match		80.0%; Score 36; DB 7; Length 453;	
Best Local Similarity		75.0%; Pred. No. 87;	
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			

QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
DB							
RESULT 28							
ABM81716							
ID	ABM81716 standard; protein; 453 AA.						
XX							
AC	ABM81716;						
XX							
DT	18-NOV-2004 (first entry)						
XX							
DE	Tumour-associated antigenic target (TAT) polypeptide PRO3640, SEQ:4422.						
XX							
XX	Tumour-associated antigenic target; TAT; human; overexpression; cancer;						
KW	tumour; diagnosis; cell proliferative disorder; breast cancer;						
KW	colorectal cancer; lung cancer; ovarian cancer; liver cancer;						
KW	central nervous system cancer; bladder cancer; pancreatic cancer;						
KW	cervical cancer; melanoma; leukaemia; hybridisation probe;						
KW	chromosome identification; chromosome mapping; gene mapping;						
KW	gene therapy; cytostatic.						
XX							
OS	Homo sapiens.						
XX							
PN	WO2004030615-A2.						
XX							
XX	15-APR-2004.						
PD							
XX							
XX	29-SEP-2003; 2003WO-US028547.						
PF							
XX							
XX	02-OCT-2002; 2002US-0414971P.						
PR							
XX							
XX	(GETH ) GENENTECH INC.						
PA							
XX							
PI	Wu TD, Zhang Z, Zhou Y;						
XX							
XX	WPI; 2004-347921/32.						
DR	N-PSDB; ACN39949.						
XX							
XX	New tumor-associated antigenic target polypeptides and nucleic acids,						
PT	useful in preparing a medicament for treating or detecting a						
PT	proliferative disorder, e.g. breast, lung, colorectal, ovarian or						
PT	prostate cancer or tumor.						
XX							
XX	Claim 12; SEQ ID NO 4422; 7273pp; English.						
PS							
XX							
CC	The invention relates to human tumour-associated antigenic target (TAT)						
CC	polypeptides, and their related nucleic acids. The TAT polypeptides are						
CC	overexpressed in cancer tissues compared to normal tissues, and may thus						
CC	serve as effective targets for the diagnosis and treatment of cancer in						
CC	mammals. The invention also relates to nucleic acid and polypeptide						
CC	sequences at least 80% identical to the TAT nucleic acids and						
CC	polypeptides; expression vectors and host cells comprising a TAT nucleic						
CC	acid; an antibody specific for a TAT polypeptide; a peptide or organic						
CC	molecule which binds to a TAT polypeptide; fusion proteins comprising a						
CC	TAT polypeptide; and methods and compositions for the treatment or						
CC	diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,						
CC	antibodies, antagonists, binding molecules and compositions are useful						
CC	for diagnosing or treating a cell proliferative disorder associated with						
CC	increased TAT expression, particularly cancers such as breast cancer,						
CC	colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder						
CC	cancer, pancreatic cancer, cervical cancer, cancers of the central						
CC	nervous system, melanoma and leukaemia. TAT nucleic acids may further be						
CC	used as hybridisation probes, in chromosome and gene mapping, in						
CC	chromosome identification and in gene therapy. The present sequence						
CC	represents a TAT polypeptide of the invention						
XX							
XX	Sequence 453 AA;						
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 453;
DB			Best Local Similarity	75.0%;	Pred. No. 87;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20					
DB							
RESULT 30							
QY	1 FYSLKIVP 8      :	13 FYSLKVP 20	Query Match	80.0%;	Score 36;	DB 4;	Length 468;
DB			Best Local Similarity	75.0%;	Pred. No. 90;		
RESULT 30			Matches	6; Conservative	1; Mismatches		

AAW37061  
ID AAW37061 standard; protein; 469 AA.  
XX AC AAW37061;  
XX  
DT 17-OCT-2003 (revised)  
DT 20-JUL-1998 (first entry)  
XX  
DE HIV-1 breakthrough isolate clone C7.10 gp120 polypeptide.  
XX  
KW HIV-1; envelope protein; gp120; MN-rgp120; vaccine; AIDS.  
XX  
OS Human immunodeficiency virus 1.  
XX  
FN WO9801564-A1.  
XX  
PD 15-JAN-1998.  
XX  
PF 03-JUL-1997; 97WO-US009690.  
XX  
PR 08-JUL-1996; 96US-0676737P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Berman PW;  
XX  
DR WPI; 1998-101059/09.  
DR N-PSDB; AAW00524.  
XX  
XX Human immunodeficiency virus gp120 sequences from vaccine breakthrough strains - useful in providing added protection against HIV not provided by original vaccine.  
PS Claim 1; Page 121-123; 193pp; English.  
XX  
CC This is the deduced sequence of a gp120 envelope polypeptide of clone C7.10 of a HIV-1 breakthrough isolate obtained from an individual infected with HIV-1 through high risk activity while participating in Phase 1 or Phase 2 trials of MN-rgp120, a candidate recombinant gp120 HIV-1 vaccine. Nucleotide sequences (see AAW00517-30) for gp120 polypeptides (see AAW37054-67) were obtained from 2 clones of each of 7 breakthrough isolates. All 7 envelope glycoproteins have sequences typical of subtype (clade) B viruses. The overall homology with MN-rgp120 is 69-80%. Use of the gp120 polypeptides from one or more of the breakthrough isolates, usually together with MN-rgp120, can provide protection against HIV strains that are sufficiently different from the vaccine strain (e.g. MN-rgp120) that the vaccine does not confer protection against those strains. The gp120 proteins can also be used in screening assays to identify antagonists of CC-CKR chemokine receptors. Antibodies induced by the polypeptides are also provided. (Updated on 17-OCT-2003 to standardise OS field)  
XX  
SQ Sequence 469 AA;  
Query Match 80.0%; Score 36; DB 2; Length 469;  
Best Local Similarity 77.8%; Pred. No. 91;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 FYSLKIVPI 9  
DB 140 FYKLNIVPI 148  
RESULT 31  
AAE39552  
ID AAE39552 standard; protein; 469 AA.  
XX  
AC AAE39552;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE HIV gp120 protein from C7.10 clone.  
XX

KW Envelope glycoprotein; gp120 protein; human immunodeficiency virus; HIV; immunogenic; vaccine.  
XX  
OS Human immunodeficiency virus.  
XX  
FH Key  
FT Region Location/Qualifiers  
FT Region 1..89  
FT Region /note= "Conserved region 1"  
FT Region 90..120  
FT Region /note= "Variable region 1"  
FT Region 121..158  
FT Region /note= "Variable region 2"  
FT Region 159..257  
FT Region /note= "Conserved region 2"  
FT Region 258..292  
FT Region /note= "Variable region 3"  
FT Region 293..337  
FT Region /note= "Conserved region 3"  
FT Region 346..403  
FT Region /note= "Conserved region 4 and variable region 4"  
FT Region 417..432  
FT Region /note= "Variable region 5"  
FT Region 433..469  
FT Region /note= "Conserved region 5"  
XX  
PN US6585979-B1.  
XX  
XX 01-JUL-2003.  
XX  
XX 15-OCT-1999; 99US-00419362.  
XX  
XX 08-JUL-1997; 97US-00899841.  
XX 17-DEC-1997; 97US-0069891P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX Berman PW;  
XX  
XX WPI; 2003-707284/67.  
XX N-PSDB; AAD60066.  
XX  
XX An immunogenic composition, useful as a vaccine against HIV, comprises a polypeptide having a gp120 MN sequence and a polypeptide having a breakthrough isolate gp120, in a carrier.  
XX  
XX Claim 1; Col 27-31; 117pp; English.  
XX  
XX The present invention relates to envelope glycoproteins (gp120) proteins from breakthrough isolates of human immunodeficiency virus (HIV) trials. The invention also relates to an immunogenic composition comprising a gp120 MN sequence and a polypeptide having a breakthrough isolate gp120, in a carrier. The composition is useful as a vaccine against HIV. The present sequence is HIV gp120 protein  
XX  
SQ Sequence 469 AA;  
Query Match 80.0%; Score 36; DB 7; Length 469;  
Best Local Similarity 77.8%; Pred. No. 91;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 FYSLKIVPI 9  
DB 140 FYKLNIVPI 148  
RESULT 32  
ADK19359  
ID ADK19359 standard; protein; 469 AA.  
XX  
AC ADK19359;  
XX  
DT 03-JUN-2004 (first entry)  
XX

DE HIV DNA gp120 clone C7.10.  
 XX  
 KW HIV; gp120; envelope glycoprotein; AIDS; vaccine; breakthrough isolate;  
 KW gp120 MN; gp120 A244; gp120 MN-GNE6; gp120 MN-GNE8; recombinant gp120;  
 KW HIV infection.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 PN US2004052821-A1.  
 XX  
 FN 18-MAR-2004.  
 XX  
 PD 21-FEB-2003; 2003US-00371472.  
 XX  
 PF 08-JUL-1996; 96US-0069891P.  
 XX  
 PR 08-JUL-1997; 97US-00889841.  
 PR 15-OCT-1999; 99US-00419362.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Berman PW;  
 FI  
 XX WPI; 2004-247705/23.  
 DR N-P8DB; ADK19358.  
 DR  
 XX New isolated human immunodeficiency virus envelope polypeptides and  
 PT oligonucleotides encoding the gp120 glycoproteins, useful for diagnosing,  
 PT preventing or treating human immunodeficiency virus (HIV) infection.  
 XX  
 PS Claim 6; SEQ ID NO 23; 126pp; English.  
 XX  
 CC The invention relates to an isolated polypeptide comprising an HIV (human  
 CC immunodeficiency virus) gp120 (envelope glycoprotein 120) amino acid  
 CC sequence and its fragment from a breakthrough isolate HIV strain isolated  
 CC from a vaccinee vaccinated with the first HIV gp120 polypeptide sequence  
 CC comprises gp120 MN, gp120 A244, gp120 MN-GNE6 or gp120 MN-GNE8  
 CC (recombinant gp120). Also included are an oligonucleotide of not more  
 CC than 5 kilobases encoding the HIV gp120 polypeptide sequence, a vaccine  
 CC comprising gp120 MN and the HIV gp120 polypeptide sequence (or fragment)  
 CC in a suitable carrier and preparing an HIV vaccine (comprising adding an  
 CC HIV gp120 polypeptide sequence or its fragments from a breakthrough  
 CC isolate from a vaccinee to the vaccine with which the vaccinee was  
 CC vaccinated). The composition and methods are useful for diagnosing,  
 CC preventing or treating HIV infection (AIDS). NOTE: The authors have mixed  
 CC up the SEQ ID numbers between the sequence listing and the  
 CC description/claims, subsequently some sequences are claimed which may not  
 CC have been intended to be claimed and some sequences which were intended  
 CC to be claimed are not claimed, other sequences cannot be identified from  
 CC the information given in the patent. The present sequence represents a  
 CC gp120 protein from a breakthrough isolate HIV strain.  
 XX  
 SQ Sequence 469 AA;  
 Query Match 80.0%; Score 36; DB 8; Length 469;  
 Best Local Similarity 77.8%; Pred. No. 91;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 FYSLKIVPI 9  
 Db 140 FYKLIVPI 148  
 XX  
 RESULT 33  
 AAW99862  
 ID AAW99862 standard; peptide; 15 AA.  
 XX  
 AC AAW99862;  
 XX  
 XX 17-OCT-2003 (revised)  
 DT 09-JUN-1999 (first entry)  
 XX  
 DE HIV-1 gp120 V1/V2 domain peptide p8.  
 XX

KW HIV-1; gp120; V1/V2 domain; human immunodeficiency virus; epitope;  
 KW infection; antibody; immunoassay.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 PN WO9912556-A1.  
 XX  
 FN 18-MAR-1999.  
 PD  
 PF 08-SEP-1998; 98WO-US018679.  
 XX  
 PR 08-SEP-1997; 97US-0058155P.  
 XX  
 XX (PUBL-) PUBLIC HEALTH RES INST NEW YORK.  
 PA (PINT/) PINTER A.  
 XX  
 PI Pinter A;  
 XX  
 DR WPI; 1999-229137/19.  
 XX  
 FN New gp120 V1/V2 fusion proteins.  
 PT  
 PS Disclosure; Page 18; 64pp; English.  
 XX  
 CC The present invention describes a novel protein (A) comprising a gp120  
 CC V1/V2 domain of an HIV-1 strain and not comprising the gp120 V3 domain of  
 CC an HIV-1 strain, where the protein does not bind CD4, the gp120 V1/V2  
 CC domain of the protein displaying an epitope which is recognized by an  
 CC antibody which neutralizes at least one HIV-1 primary isolate with a ND90  
 CC of at most 100 mu g/ml. The present sequence represents an HIV-1 gp120  
 CC V1/V2 domain peptide from the present invention. The novel proteins can  
 CC be used for stimulating the formation of antibodies capable of  
 CC neutralizing infection by an HIV viral isolate in mammals. They can also  
 CC be used for therapeutic treatment of subjects already infected with HIV.  
 CC They can also be used in immunoassays for anti-HIV antibodies and for the  
 CC production of anti-HIV antiserum. (Updated on 17-OCT-2003 to standardise  
 CC OS field)  
 XX  
 SQ Sequence 15 AA;  
 Query Match 77.8%; Score 35; DB 2; Length 15;  
 Best Local Similarity 77.8%; Pred. No. 3.6;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 FYSLKIVPI 9  
 Db 5 FYKLIVPI 13  
 XX  
 RESULT 34  
 AAW99851  
 ID AAW99851 standard; peptide; 34 AA.  
 XX  
 AC AAW99851;  
 XX  
 DT 17-OCT-2003 (revised)  
 DT 09-JUN-1999 (first entry)  
 XX  
 DE HIV-1 gp120 V1/V2 domain peptide #1.  
 XX  
 KW HIV-1; gp120; V1/V2 domain; human immunodeficiency virus; epitope;  
 KW infection; antibody; immunoassay.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 PN WO9912556-A1.  
 XX  
 FN 18-MAR-1999.  
 PD  
 PF 08-SEP-1998; 98WO-US018679.  
 XX  
 PR 08-SEP-1997; 97US-0058155P.  
 XX



PA (PUBL-) PUBLIC HEALTH RES INST NEW YORK.  
 PA (PINT/) PINTER A.  
 XX Pinter A;  
 XX WPI; 1999-229137/19.  
 XX New gp120 V1/V2 fusion proteins.  
 XX Claim 11; Page 42; 64pp; English.  
 PS  
 XX The present invention describes a novel protein (A) comprising a gp120  
 CC V1/V2 domain of an HIV-1 strain and not comprising the gp120 V3 domain of  
 CC an HIV-1 strain, where the protein does not bind CD4, the gp120 V1/V2  
 CC domain of the protein displaying an epitope which is recognized by an  
 CC antibody which neutralizes at least one HIV-1 primary isolate with a ND90  
 CC of at most 100 mu g/ml. The present sequence represents an HIV-1 gp120  
 CC V1/V2 domain peptide from the present invention. The novel proteins can  
 CC be used for stimulating the formation of antibodies capable of  
 CC neutralizing infection by an HIV viral isolate in mammals. They can also  
 CC be used for therapeutic treatment of subjects already infected with HIV.  
 CC They can also be used in immunoassays for anti-HIV antibodies and for the  
 CC production of anti-HIV antiserum. (Updated on 17-OCT-2003 to standardise  
 CC OS field)  
 CC  
 XX Sequence 34 AA;  
 SQ  
 Query Match 77.8%; Score 35; DB 2; Length 34;  
 Best Local Similarity 77.8%; Pred. No. 8.7;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 FYSLXIVPI 9  
 DB 25 FYKLDIVPI 33  
 ||| ||||  
 RESULT 35  
 AAB10710  
 ID AAB10710 standard; protein; 51 AA.  
 AC AAB10710;  
 XX  
 DT 12-SEP-2003 (revised)  
 DT 26-JAN-2001 (first entry)  
 XX  
 DE HIV-1 gp120 protein NL4-3 V2 loop region fragment.  
 XX  
 KW Viral protein; vaccine; anti-viral; anti-HIV; therapy; infection; gp120;  
 KW V2 loop.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 PN WO200047223-A2.  
 PD 17-AUG-2000.  
 XX  
 PF 03-DEC-1999; 99WO-EP009759.  
 XX  
 PR 12-FEB-1999; 99DE-01007485.  
 XX  
 PA (STPA-) STRATHMANN & CO AG.  
 XX  
 PI Schreiber M;  
 XX  
 DR WPI; 2000-549084/50.  
 XX  
 PT Viral vaccine comprises a mixture of protein sequence variants of a  
 PT single viral protein, which is useful for prevention and therapy of viral  
 PT infections, especially HIV, in humans.  
 XX  
 PS Disclosure; Fig 2a; 79pp; German.  
 XX  
 CC This invention describes a novel protein vaccine which comprises a

CC mixture of viral proteins, characterized in that the molecules are  
 CC sequence variants of a single viral (partial) protein. The products of  
 CC the invention have anti-viral and anti-HIV activity. Mixtures of  
 CC structurally different viral proteins, that are sequence variants of a  
 CC single protein are useful for production of vaccines for the prevention  
 CC and/or therapy of viral infections in humans. The vaccines are especially  
 CC useful for prevention and/or therapy of human immunodeficiency virus  
 CC (HIV) infection in humans. The vectors and host cells are useful for the  
 CC expression of the protein/DNA mixtures, which are also useful for  
 CC preventing and/or therapy of viral infection. This sequence represents a  
 CC HIV-1 gp120 protein V2 loop fragment. (Updated on 12-SEP-2003 to  
 CC standardise OS field)  
 XX  
 SQ Sequence 51 AA;  
 Query Match 77.8%; Score 35; DB 3; Length 51;  
 Best Local Similarity 77.8%; Pred. No. 13;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 FYSLXIVPI 9  
 DB 25 FYKLDIVPI 33  
 ||| ||||  
 RESULT 36  
 ABP52850  
 ID ABP52850 standard; peptide; 78 AA.  
 AC ABP52850;  
 XX  
 DT 29-AUG-2003 (revised)  
 DT 02-NOV-2002 (first entry)  
 XX  
 DE HIV-1 gp120 V2 region related peptide SEQ ID NO:19.  
 XX  
 KW HIV; transgenic mouse; human monoclonal antibody; neutralising; HIV-1;  
 KW gp120; anti-HIV; gene therapy; antibody; glycoprotein 120; infection.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 PN WO200259154-A2.  
 PD 01-AUG-2002.  
 XX  
 PF 25-JAN-2002; 2002WO-US002171.  
 XX  
 PR 26-JAN-2001; 2001US-0264398P.  
 PR 02-FEB-2001; 2001US-0266106P.  
 PR 03-FEB-2001; 2001US-0265984P.  
 PR 21-FEB-2001; 2001US-0270466P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 PA (PUBL-) PUBLIC HEALTH RES INST.  
 XX  
 PI Pinter A, He Y, Corvalan JR;  
 XX  
 DR WPI; 2002-627409/67.  
 XX  
 PT Isolated human antibody or its antigen-binding portion that specifically  
 PT binds to human deficiency virus-1 glycoprotein 120 and that has HIV-1  
 PT neutralizing activity, useful to treat or prevent HIV-1 infection.  
 XX  
 PS Disclosure; Page 12; 163pp; English.  
 XX  
 CC The present invention describes an isolated human antibody (I) or its  
 CC antigen-binding portion that specifically binds to human immunodeficiency  
 CC virus (HIV)-1 glycoprotein (gp)120 protein and that has HIV-1  
 CC neutralising activity, where (I) or its antigen-binding portion  
 CC recognises an epitope on a V1/V2 domain of HIV-1 gp120, where the epitope  
 CC is dependent on the presence of a sequence in the V1 loop. (I) has anti-  
 CC HIV activity and can be used in gene therapy. (I) is useful for treating,  
 CC preventing or inhibiting HIV-1 infection in a subject or for preventing  
 CC or lessening the severity of a condition caused by HIV-1 infection in a

CC subject, by administering (I) to the subject. (I) is useful for  
 CC inhibiting HIV-1 virus binding to a T-cell, or for inhibiting HIV-1 virus  
 CC infection of a T-cell, by contacting the virus with (I). (I) is useful  
 CC for inhibiting HIV-1 gp120-mediated binding by contacting a gp120-  
 CC expressing HIV-1 virus with (I). (I) is useful diagnostically to detect  
 CC the presence of HIV-1 virus in a subject. The present sequence represents  
 CC an HIV-1 V2 region related peptide, which is used in the exemplification  
 CC of the present invention. (Updated on 29-AUG-2003 to standardise OS  
 CC field)  
 XX  
 SQ Sequence 78 AA;

Query Match 77.8%; Score 35; DB 5; Length 78;  
 Best Local Similarity 77.8%; Pred. No. 21;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
 |||||  
 Db 56 FYKLDIVPI 64

RESULT 37  
 AAW99852  
 ID AAW99852 standard; peptide; 96 AA.  
 XX  
 AC AAW99852;

XX 17-OCT-2003 (revised)  
 DT 09-JUN-1999 (first entry)  
 XX

XX HIV-1 gp120 V1/V2 domain peptide SEQ ID NO:1.

XX HIV-1; gp120; V1/V2 domain; human immunodeficiency virus; epitope;  
 KW infection; antibody; immunoassay.

XX Human immunodeficiency virus 1.

XX WO9912556-A1.

XX 18-MAR-1999.

XX 08-SEP-1998; 98WO-US018679.

XX 08-SEP-1997; 97US-0058155P.

XX (PUBL-) PUBLIC HEALTH RES INST NEW YORK.

XX (PINT/) PINTER A.

XX Pinter A;

XX WPI; 1999-229137/19.

XX New gp120 V1/V2 fusion proteins.

XX Claim 14; Page 42; 64pp; English.

XX The present invention describes a novel protein (A) comprising a gp120  
 CC V1/V2 domain of an HIV-1 strain and not comprising the gp120 V3 domain of  
 CC an HIV-1 strain, where the protein does not bind CD4, the gp120 V1/V2  
 CC domain of the protein displaying an epitope which is recognized by an  
 CC antibody which neutralizes at least one HIV-1 primary isolate with a ND90  
 CC of at most 100 µg/ml. The present sequence represents an HIV-1 gp120  
 CC V1/V2 domain peptide from the present invention. The novel proteins can  
 CC be used for stimulating the formation of antibodies capable of  
 CC neutralizing infection by an HIV viral isolate in mammals. They can also  
 CC be used for therapeutic treatment of subjects already infected with HIV.  
 CC They can also be used in immunoassays for anti-HIV antibodies and for the  
 CC production of anti-HIV antiserum. (Updated on 17-OCT-2003 to standardise  
 CC OS field)

XX Sequence 96 AA;

Query Match 77.8%; Score 35; DB 2; Length 96;

Best Local Similarity 77.8%; Pred. No. 27;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
 |||||  
 Db 66 FYKLDIVPI 74

RESULT 38  
 ABP78185  
 ID ABP78185 standard; protein; 245 AA.  
 XX

XX ABP78185;

XX 07-MAR-2003 (first entry)

XX N. gonorrhoeae amino acid sequence SEQ ID 2900.

XX Antibacterial; infection; vaccine; gene therapy.

XX Neisseria gonorrhoeae.

XX WO200279243-A2.

XX 10-OCT-2002.

XX 12-FEB-2002; 2002WO-IB002069.

XX 12-FEB-2001; 2001GB-00003424.

XX (CHIR-) CHIRON SPA.

XX Fontana MR, Pizza M, Massignani V, Monaci E;

XX WPI; 2003-058415/05.

XX N-PSDB; ABZ39155.

XX New protein from Neisseria gonorrhoeae, useful for the manufacture of a  
 PT medicament for treating or preventing N. gonorrhoeae infection.

XX Disclosure; Page 400; 815pp; English.

XX The present invention relates to proteins from Neisseria gonorrhoeae.  
 CC Also disclosed are the nucleic acid molecules encoding the proteins and  
 CC antibodies that specifically bind to the proteins. The composition  
 CC comprising the protein, nucleic acid or antibody is useful for the  
 CC manufacture of a medicament for treating or preventing N. gonorrhoeae  
 CC infection, this may be in the form of a vaccine or gene therapy.

XX Sequences given in records ABP76736-ABP81046 represent nucleic acid  
 CC molecules of the invention

XX Sequence 245 AA;

Query Match 77.8%; Score 35; DB 6; Length 245;

Best Local Similarity 55.6%; Pred. No. 73;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
 |||||  
 Db 179 FYSPKLLPV 187

RESULT 39  
 ABU37576

ID ABU37576 standard; protein; 245 AA.

XX ABU37576;

XX 23-OCT-2003 (revised)

DT 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #23103.

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX Neisseria gonorrhoeae.  
OS  
XX WO200277183-A2.  
PN  
XX 03-OCT-2002.  
XX  
XX 21-MAR-2002; 2002WO-US009107.  
XX  
XX 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
XX (ELIT-) ELITRA PHARM INC.  
PA Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
PI  
XX WPI; 2003-029926/02.  
DR N-PSDB; ACA11446.  
XX  
XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
XX Claim 25; SEQ ID NO 65500; 1766pp; English.  
XX  
XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway;  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences. (Updated on 23-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 245 AA;

Query Match 77.8%; Score 35; DB 6; Length 245;  
Best Local Similarity 55.6%; Pred. No. 73;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
||| |::|  
DB 179 FYSFKLLPV 187

## RESULT 40

ADP08243  
ID ADP08243 standard; protein; 245 AA.

XX AC ADP08243;

XX DT 26-AUG-2004 (first entry)

XX DE Neisseria meningitidis MC58 OMV-related membrane protein - SEQ ID 76.

XX KW outer-membrane vesicle; antibacterial; antiinflammatory;  
KW meningococcal protein trafficking; localisation; infection; vaccine;  
KW gene therapy.

XX OS Neisseria meningitidis MC58.

XX PN WO2004046177-A2.

XX PD 03-JUN-2004.

XX PF 17-NOV-2003; 2003WO-IB006281.

XX PR 15-NOV-2002; 2002GB-00026734.

XX PR 27-MAR-2003; 2003GB-00007131.

XX PA (CHTR ) CHIRON SRL.

XX PI Norais N, Grandi G;

XX DR WPI; 2004-420615/39.

XX PT New compositions having outer-membrane vesicles and proteins from  
PT Neisseria meningitidis, useful in the field of meningococcal  
PT biochemistry, in particular for preventing and/or treating meningococcal  
PT infections.

XX PS Claim 9; SEQ ID NO 76; 79pp; English.

XX The invention relates to a novel composition comprising outer-membrane  
CC vesicles (OMV) prepared from a first strain of *Neisseria meningitidis* and  
CC 1 or more proteins which are present in OMVs prepared from a second  
CC strain of *N. meningitidis*, but which are not present in OMVs prepared  
CC from the first strain. The composition of the invention demonstrates  
CC antibacterial and antiinflammatory activities and may be useful in the  
CC field of meningococcal biochemistry, in particular the trafficking and  
CC localisation of meningococcal proteins, as well as in the prevention or  
CC treatment of meningococcal infections, possibly via the production of a  
CC vaccine or gene therapy. The current sequence is that of a *Neisseria*  
CC meningitidis MC58 outer-membrane vesicle (OMV)-related membrane protein  
CC of the invention.

XX SQ Sequence 245 AA;

Query Match 77.8%; Score 35; DB 8; Length 245;

Best Local Similarity 55.6%; Pred. No. 73;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
||| |::|

DB 179 FYSFKLLPV 187

Search completed: February 24, 2005, 19:11:39  
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Gapop 10.0 , Gapext 0.5

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Maximum Match 100%

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2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/ECTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	9	US-09-256-194-5	Sequence 5, Appli
2	39	86.7	43	US-09-536-977-6	Sequence 6, Appli
3	39	86.7	168	US-09-536-977-42	Sequence 42, Appl
4	39	86.7	425	US-09-536-977-46	Sequence 46, Appl
5	39	86.7	425	US-09-536-977-48	Sequence 48, Appl
6	39	86.7	425	US-09-536-977-50	Sequence 50, Appl
7	39	86.7	425	US-09-536-977-52	Sequence 52, Appl
8	39	86.7	476	US-09-536-977-74	Sequence 74, Appl
9	39	86.7	635	US-09-536-977-68	Sequence 68, Appl
10	39	86.7	657	US-09-256-194-2	Sequence 2, Appli
11	39	86.7	687	US-09-536-977-70	Sequence 70, Appl
12	39	86.7	820	US-09-536-977-72	Sequence 72, Appl
13	38	84.4	498	US-08-889-841B-2	Sequence 2, Appli
14	38	84.4	498	US-08-889-841B-5	Sequence 5, Appli
15	38	84.4	498	US-09-419-362-2	Sequence 2, Appli
16	38	84.4	498	US-09-419-362-5	Sequence 5, Appli
17	36	80.0	131	US-09-513-999C-5328	Sequence 5328, Ap
18	36	80.0	454	US-09-949-016-11717	Sequence 11717, A
19	36	80.0	469	US-08-889-841B-23	Sequence 23, Appl
20	36	80.0	469	US-09-419-362-23	Sequence 23, Appl
21	35	77.8	15	US-10-038-407-16	Sequence 16, Appl
22	35	77.8	34	US-10-038-407-2	Sequence 2, Appli
23	35	77.8	96	US-10-038-407-1	Sequence 1, Appli
24	35	77.8	365	US-10-038-407-28	Sequence 28, Appl
25	35	77.8	473	US-09-438-917-6	Sequence 6, Appli
26	35	77.8	494	US-08-889-841B-19	Sequence 19, Appl
27	35	77.8	494	US-09-419-362-19	Sequence 19, Appl

28 35 77.8 495 3 US-08-889-841B-25 Sequence 25, Appli  
29 35 77.8 495 3 US-08-889-841B-28 Sequence 28, Appli  
30 35 77.8 495 4 US-09-419-362-25 Sequence 25, Appli  
31 35 77.8 495 4 US-09-419-362-28 Sequence 28, Appli  
32 35 77.8 587 4 US-09-646-028-50 Sequence 50, Appli  
33 35 77.8 595 4 US-09-646-028-56 Sequence 56, Appli  
34 35 77.8 601 4 US-09-646-028-52 Sequence 52, Appli  
35 35 77.8 826 1 US-08-375-510-2 Sequence 2, Appli  
36 35 77.8 826 2 US-08-487-657-2 Sequence 2, Appli  
37 35 77.8 854 4 US-09-309-572-23 Sequence 23, Appli  
38 35 77.8 854 4 US-09-718-096-23 Sequence 13, Appli  
39 34 75.6 28 2 US-08-493-235-13 Sequence 13, Appli  
40 34 75.6 28 4 US-10-038-407-6 Sequence 6, Appli  
41 34 75.6 93 4 US-10-038-407-3 Sequence 3, Appli  
42 34 75.6 99 4 US-09-248-796A-22816 Sequence 22816, A  
43 34 75.6 358 4 US-09-438-917-19 Sequence 19, Appli  
44 34 75.6 429 4 US-09-438-917-16 Sequence 16, Appli  
45 34 75.6 455 3 US-08-889-841B-46 Sequence 46, Appli

#### ALIGNMENTS

#### RESULT 1

US-09-256-194-5  
; Sequence 5, Application US/09256194  
; Patent No. 6395714  
; GENERAL INFORMATION:  
; APPLICANT: Sia, Charles D.Y.  
; APPLICANT: Cao, Shi Xian  
; APPLICANT: Persson, Roy  
; APPLICANT: Rovinski, Benjamin  
; TITLE OF INVENTION: EXPRESSING GP140 FRAGMENT OF PRIMARY HIV-1 ISOLATE  
; FILE REFERENCE: 1038-920  
; CURRENT APPLICATION NUMBER: US/09/256,194  
; CURRENT FILING DATE: 1999-02-24  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-256-194-5

Query Match 100.0%; Score 45; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVSLKIVPI 9

Db 1 FVSLKIVPI 9

#### RESULT 2

US-09-536-977-6  
; Sequence 6, Application US/09536977  
; Patent No. 6649409  
; GENERAL INFORMATION:  
; APPLICANT: FOMSGAARD, ANDERS  
; TITLE OF INVENTION: METHOD FOR PRODUCING A NUCLEOTIDE SEQUENCE CONSTRUCT  
; TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED  
; TITLE OF INVENTION: ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE  
; TITLE OF INVENTION: BX08 CONSTRUCTS  
; FILE REFERENCE: 030307/0169  
; CURRENT APPLICATION NUMBER: US/09/536,977  
; CURRENT FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60/128,558  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: DK PA1999 00427  
; PRIOR FILING DATE: 1999-03-29  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6

```
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-536-977-6

Query Match      86.7%; Score 39; DB 4; Length 43;
Best Local Similarity 88.9%; Pred. No. 0.44;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
      ||||| |||||
Db      20 FYSLDIVPI 28

RESULT 3
US-09-536-977-42
; Sequence 42, Application US/09536977
; Patent No. 6649409
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; TITLE OF INVENTION: METHOD FOR PRODUCING A NUCLEOTIDE SEQUENCE CONSTRUCT
; TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED
; TITLE OF INVENTION: ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
; FILE REFERENCE: 030307/0169
; CURRENT APPLICATION NUMBER: US/09/536,977
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/128,558
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: DK PA1999 00427
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-536-977-42

Query Match      86.7%; Score 39; DB 4; Length 168;
Best Local Similarity 88.9%; Pred. No. 1.9;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
      ||||| |||||
Db      145 FYSLDIVPI 153

RESULT 4
US-09-536-977-46
; Sequence 46, Application US/09536977
; Patent No. 6649409
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; TITLE OF INVENTION: METHOD FOR PRODUCING A NUCLEOTIDE SEQUENCE CONSTRUCT
; TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED
; TITLE OF INVENTION: ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
; FILE REFERENCE: 030307/0169
; CURRENT APPLICATION NUMBER: US/09/536,977
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/128,558
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: DK PA1999 00427
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-536-977-46

Query Match      86.7%; Score 39; DB 4; Length 425;
Best Local Similarity 88.9%; Pred. No. 5;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
      ||||| |||||
Db      145 FYSLDIVPI 153

RESULT 5
US-09-536-977-48
; Sequence 48, Application US/09536977
; Patent No. 6649409
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; TITLE OF INVENTION: METHOD FOR PRODUCING A NUCLEOTIDE SEQUENCE CONSTRUCT
; TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED
; TITLE OF INVENTION: ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
; FILE REFERENCE: 030307/0169
; CURRENT APPLICATION NUMBER: US/09/536,977
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/128,558
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: DK PA1999 00427
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-536-977-48

Query Match      86.7%; Score 39; DB 4; Length 425;
Best Local Similarity 88.9%; Pred. No. 5;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
      ||||| |||||
Db      145 FYSLDIVPI 153

RESULT 6
US-09-536-977-50
; Sequence 50, Application US/09536977
; Patent No. 6649409
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; TITLE OF INVENTION: METHOD FOR PRODUCING A NUCLEOTIDE SEQUENCE CONSTRUCT
; TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED
; TITLE OF INVENTION: ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
; FILE REFERENCE: 030307/0169
; CURRENT APPLICATION NUMBER: US/09/536,977
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/128,558
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: DK PA1999 00427
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-536-977-50

Query Match      86.7%; Score 39; DB 4; Length 425;
Best Local Similarity 88.9%; Pred. No. 5;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
      ||||| |||||
Db      145 FYSLDIVPI 153
```

```
Db      145 FYSLDIVPI 153

RESULT 7
US-09-536-977-52
; Sequence 52, Application US/09536977
; Patent No. 6649409
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; TITLE OF INVENTION: METHOD FOR PRODUCING A NUCLEOTIDE SEQUENCE CONSTRUCT
; TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED
; TITLE OF INVENTION: ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
; FILE REFERENCE: 030307/0169
; CURRENT APPLICATION NUMBER: US/09/536,977
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/128,558
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: DK PA1999 00427
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-536-977-52
Query Match      86.7%; Score 39; DB 4; Length 425;
Best Local Similarity 88.9%; Pred. No. 5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
Db      145 FYSLDIVPI 153

RESULT 8
US-09-536-977-74
; Sequence 74, Application US/09536977
; Patent No. 6649409
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; TITLE OF INVENTION: METHOD FOR PRODUCING A NUCLEOTIDE SEQUENCE CONSTRUCT
; TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED
; TITLE OF INVENTION: ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
; FILE REFERENCE: 030307/0169
; CURRENT APPLICATION NUMBER: US/09/536,977
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/128,558
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: DK PA1999 00427
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-536-977-74
Query Match      86.7%; Score 39; DB 4; Length 476;
Best Local Similarity 88.9%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
Db      145 FYSLDIVPI 153

RESULT 9
US-09-536-977-68
; Sequence 68, Application US/09536977
; Patent No. 6649409
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; TITLE OF INVENTION: METHOD FOR PRODUCING A NUCLEOTIDE SEQUENCE CONSTRUCT
; TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED
; TITLE OF INVENTION: ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
; FILE REFERENCE: 030307/0169
; CURRENT APPLICATION NUMBER: US/09/536,977
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/128,558
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: DK PA1999 00427
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 635
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-536-977-68
Query Match      86.7%; Score 39; DB 4; Length 635;
Best Local Similarity 88.9%; Pred. No. 7.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
Db      145 FYSLDIVPI 153

RESULT 10
US-09-256-194-2
; Sequence 2, Application US/09256194
; Patent No. 6395714
; GENERAL INFORMATION:
; APPLICANT: Sia, Charles D.Y.
; APPLICANT: Cao, Shi Xian
; APPLICANT: Persson, Roy
; APPLICANT: Rovinski, Benjamin
; TITLE OF INVENTION: EXPRESSING GP140 FRAGMENT OF PRIMARY HIV-1 ISOLATE
; FILE REFERENCE: 1038-920
; CURRENT APPLICATION NUMBER: US/09/256,194
; CURRENT FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 657
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-256-194-2
Query Match      86.7%; Score 39; DB 3; Length 657;
Best Local Similarity 88.9%; Pred. No. 7.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
Db      162 FYSLDIVPI 170

RESULT 11
US-09-536-977-70
; Sequence 70, Application US/09536977
; Patent No. 6649409
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; TITLE OF INVENTION: METHOD FOR PRODUCING A NUCLEOTIDE SEQUENCE CONSTRUCT
; TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED
; TITLE OF INVENTION: ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
; FILE REFERENCE: 030307/0169
; CURRENT APPLICATION NUMBER: US/09/536,977
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/128,558
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: DK PA1999 00427
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-536-977-70
Query Match      86.7%; Score 39; DB 4; Length 476;
Best Local Similarity 88.9%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
Db      145 FYSLDIVPI 153
```

```
; FILE REFERENCE: 030307/0169
; CURRENT APPLICATION NUMBER: US/09/536,977
; CURRENT FILING DATE: 2000-03-29
; PRIOR FILING DATE: 60/128,558
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: DK PA1999 00427
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 70
; LENGTH: 687
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-536-977-70

Query Match      86.7%; Score 39; DB 4; Length 687;
Best Local Similarity 88.9%; Pred. No. 8.3;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 FYSLKIVPI 9
   ||||| |||||
Db 145 FYSLDIVPI 153

RESULT 12
US-09-536-977-72
; Sequence 72, Application US/09536977
; Patent No. 6649409
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; TITLE OF INVENTION: METHOD FOR PRODUCING A NUCLEOTIDE SEQUENCE CONSTRUCT
; TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED
; TITLE OF INVENTION: ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
; TITLE OF INVENTION: BX08 CONSTRUCTS
; FILE REFERENCE: 030307/0169
; CURRENT APPLICATION NUMBER: US/09/536,977
; CURRENT FILING DATE: 2000-03-29
; PRIOR FILING DATE: 60/128,558
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: DK PA1999 00427
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 72
; LENGTH: 820
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-536-977-72

Query Match      86.7%; Score 39; DB 4; Length 820;
Best Local Similarity 88.9%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 FYSLKIVPI 9
   ||||| |||||
Db 145 FYSLDIVPI 153

RESULT 13
US-08-889-841B-2
; Sequence 2, Application US/08889841B
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703CIP
; CURRENT APPLICATION NUMBER: US/08/889,841B
; CURRENT FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 498
; TYPE: PRT
; ORGANISM: HIV
US-09-536-977-70

Query Match      86.7%; Score 39; DB 4; Length 820;
Best Local Similarity 88.9%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 FYSLKIVPI 9
   ||||| |||||
Db 145 FYSLDIVPI 153

RESULT 14
US-08-889-841B-5
; Sequence 5, Application US/08889841B
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703CIP
; CURRENT APPLICATION NUMBER: US/08/889,841B
; CURRENT FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 498
; TYPE: PRT
; ORGANISM: HIV
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(498)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-08-889-841B-5

Query Match      84.4%; Score 38; DB 3; Length 498;
Best Local Similarity 77.8%; Pred. No. 9.6;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 FYSLKIVPI 9
   ||||| |||||
Db 156 FYSLDVPI 164

RESULT 15
US-09-419-362-2
; Sequence 2, Application US/09419362
; Patent No. 6585979
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/09/419,362
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 498
; TYPE: PRT
; ORGANISM: HIV
US-09-419-362-2

Query Match      84.4%; Score 38; DB 4; Length 498;
Best Local Similarity 77.8%; Pred. No. 9.6;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 FYSLKIVPI 9
   ||||| |||||
```



Db 156 FYSLDVVPI 164

RESULT 16  
US-09-419-362-5  
; Sequence 5: Application US/09419362  
; Patent No. 6585979  
; GENERAL INFORMATION:  
; APPLICANT: Berman, Phillip W.  
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE  
; FILE REFERENCE: 14918-703DIV1  
; CURRENT APPLICATION NUMBER: US/09/419,362  
; CURRENT FILING DATE: 1999-10-15  
; PRIOR APPLICATION NUMBER: US 08/889,841  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: US 60/676,737  
; PRIOR FILING DATE: 1996-07-08  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 498  
; TYPE: PRT  
; ORGANISM: HIV  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(498)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-419-362-5

Query Match 84.4%; Score 38; DB 4; Length 498;  
Best Local Similarity 77.8%; Pred. No. 9.6;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
|||||:|  
Db 156 FYSLDVVPI 164

RESULT 17  
US-09-513-999C-5328  
; Sequence 5328: Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 5328  
; LENGTH: 131  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-513-999C-5328

Query Match 80.0%; Score 36; DB 4; Length 131;  
Best Local Similarity 75.0%; Pred. No. 6;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVP 8  
|||||:|  
Db 13 FYSLKVAP 20

RESULT 18  
US-09-949-016-11717  
; Sequence 11717: Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11717  
; LENGTH: 454  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-11717

Query Match 80.0%; Score 36; DB 4; Length 454;  
Best Local Similarity 75.0%; Pred. No. 23;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVP 8  
|||||:|  
Db 14 FYSLKVAP 21

RESULT 19  
US-08-889-841B-23  
; Sequence 23: Application US/08889841B  
; GENERAL INFORMATION:  
; APPLICANT: Berman, Phillip W.  
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE  
; FILE REFERENCE: 14918-703CIP  
; CURRENT APPLICATION NUMBER: US/08/889,841B  
; CURRENT FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: US 60/676,737  
; PRIOR FILING DATE: 1996-07-08  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 23  
; LENGTH: 469  
; TYPE: PRT  
; ORGANISM: HIV  
US-08-889-841B-23

Query Match 80.0%; Score 36; DB 3; Length 469;  
Best Local Similarity 77.8%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
|||||:|  
Db 140 FYKLINIVPI 148

RESULT 20  
US-09-419-362-23  
; Sequence 23: Application US/09419362  
; Patent No. 6585979  
; GENERAL INFORMATION:  
; APPLICANT: Berman, Phillip W.  
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE  
; FILE REFERENCE: 14918-703DIV1  
; CURRENT APPLICATION NUMBER: US/09/419,362  
; CURRENT FILING DATE: 1999-10-15  
; PRIOR APPLICATION NUMBER: US 08/889,841  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: US 60/676,737  
; PRIOR FILING DATE: 1996-07-08

```
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 469
; TYPE: PRT
; ORGANISM: HIV
US-09-419-362-23

Query Match      80.0%; Score 36; DB 4; Length 469;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
Db 140 FYKLIVPI 148

RESULT 21
US-10-038-407-16
; Sequence 16, Application US/10038407
; Patent No. 6815201
; GENERAL INFORMATION:
; APPLICANT: Pinter, Abraham
; TITLE OF INVENTION: HIV-1 gp120 V1/V2 DOMAIN EPITOPES
; FILE REFERENCE: 07763-048001
; CURRENT APPLICATION NUMBER: US/10/038,407
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: 09/508,208
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US98/18679
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/058,155
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus (HIV)
US-10-038-407-16

Query Match      77.8%; Score 35; DB 4; Length 15;
Best Local Similarity 77.8%; Pred. No. 0.96;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
Db 5 FYKLIVPI 13

RESULT 22
US-10-038-407-2
; Sequence 2, Application US/10038407
; Patent No. 6815201
; GENERAL INFORMATION:
; APPLICANT: Pinter, Abraham
; TITLE OF INVENTION: HIV-1 gp120 V1/V2 DOMAIN EPITOPES
; FILE REFERENCE: 07763-048001
; CURRENT APPLICATION NUMBER: US/10/038,407
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: 09/508,208
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US98/18679
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/058,155
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus (HIV)
US-10-038-407-2

Query Match      77.8%; Score 35; DB 4; Length 34;
Best Local Similarity 77.8%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
Db 25 FYKLIVPI 33

RESULT 23
US-10-038-407-1
; Sequence 1, Application US/10038407
; Patent No. 6815201
; GENERAL INFORMATION:
; APPLICANT: Pinter, Abraham
; TITLE OF INVENTION: HIV-1 gp120 V1/V2 DOMAIN EPITOPES
; FILE REFERENCE: 07763-048001
; CURRENT APPLICATION NUMBER: US/10/038,407
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: 09/508,208
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US98/18679
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/058,155
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus (HIV)
US-10-038-407-1

Query Match      77.8%; Score 35; DB 4; Length 96;
Best Local Similarity 77.8%; Pred. No. 7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
Db 66 FYKLIVPI 74

RESULT 24
US-10-038-407-28
; Sequence 28, Application US/10038407
; Patent No. 6815201
; GENERAL INFORMATION:
; APPLICANT: Pinter, Abraham
; TITLE OF INVENTION: HIV-1 gp120 V1/V2 DOMAIN EPITOPES
; FILE REFERENCE: 07763-048001
; CURRENT APPLICATION NUMBER: US/10/038,407
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: 09/508,208
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US98/18679
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/058,155
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus (HIV)
US-10-038-407-28

Query Match      77.8%; Score 35; DB 4; Length 365;
Best Local Similarity 77.8%; Pred. No. 29;
```

```
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 335 FYKLDIVPI 343

RESULT 25
US-09-438-917-6
; Sequence 6, Application US/09438917
; Patent No. 6787646
; GENERAL INFORMATION:
; APPLICANT: Immunol Incorporated
; APPLICANT: Welch, Peter J.
; APPLICANT: Barber, Jack R.
; TITLE OF INVENTION: Tumor Suppressor Molecules and Methods
; FILE REFERENCE: 039316-0301
; CURRENT APPLICATION NUMBER: US/09/438,917
; CURRENT FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 473
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-438-917-6

Query Match 77.8%; Score 35; DB 4; Length 473;
Best Local Similarity 62.5%; Pred. No. 38;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSLKIVPI 9
Db 197 YSIKVVP 204

RESULT 26
US-08-889-841B-19
; Sequence 19, Application US/08889841B
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703CIP
; CURRENT APPLICATION NUMBER: US/08/889,841B
; CURRENT FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 494
; TYPE: PRT
; ORGANISM: HIV
US-08-889-841B-19

Query Match 77.8%; Score 35; DB 3; Length 494;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 145 FYKLDIVPI 153

RESULT 27
US-09-419-362-19
; Sequence 19, Application US/09419362
; Patent No. 6585979
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
```

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; CURRENT APPLICATION NUMBER: US/09/419,362
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 494
; TYPE: PRT
; ORGANISM: HIV
US-09-419-362-19

Query Match 77.8%; Score 35; DB 4; Length 494;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 145 FYKLDIVPI 153

RESULT 28
US-08-889-841B-25
; Sequence 25, Application US/08889841B
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703CIP
; CURRENT APPLICATION NUMBER: US/08/889,841B
; CURRENT FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 495
; TYPE: PRT
; ORGANISM: HIV
US-08-889-841B-25

Query Match 77.8%; Score 35; DB 3; Length 495;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 152 FYKLDIVPI 160

RESULT 29
US-08-889-841B-28
; Sequence 28, Application US/08889841B
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703CIP
; CURRENT APPLICATION NUMBER: US/08/889,841B
; CURRENT FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 495
; TYPE: PRT
; ORGANISM: HIV
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(495)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-08-889-841B-28
```

Query Match 77.8%; Score 35; DB 3; Length 495;  
Best Local Similarity 77.8%; Pred. No. 40;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
||| ||||  
Db 152 FYKLDIVPI 160

RESULT 30  
US-09-419-362-25  
; Sequence 25, Application US/09419362  
; Patent No. 6585979  
; GENERAL INFORMATION:  
; APPLICANT: Berman, Phillip W.  
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE  
; FILE REFERENCE: 14918-703DIV1  
; CURRENT APPLICATION NUMBER: US/09/419,362  
; CURRENT FILING DATE: 1999-10-15  
; PRIOR APPLICATION NUMBER: US 08/889,841  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: US 60/676,737  
; PRIOR FILING DATE: 1996-07-08  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 495  
; TYPE: PRT  
; ORGANISM: HIV  
US-09-419-362-25

Query Match 77.8%; Score 35; DB 4; Length 495;  
Best Local Similarity 77.8%; Pred. No. 40;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
||| ||||  
Db 152 FYKLDIVPI 160

RESULT 31  
US-09-419-362-28  
; Sequence 28, Application US/09419362  
; Patent No. 6585979  
; GENERAL INFORMATION:  
; APPLICANT: Berman, Phillip W.  
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE  
; FILE REFERENCE: 14918-703DIV1  
; CURRENT APPLICATION NUMBER: US/09/419,362  
; CURRENT FILING DATE: 1999-10-15  
; PRIOR APPLICATION NUMBER: US 08/889,841  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: US 60/676,737  
; PRIOR FILING DATE: 1996-07-08  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 28  
; LENGTH: 495  
; TYPE: PRT  
; ORGANISM: HIV  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(495)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-419-362-28

Query Match 77.8%; Score 35; DB 4; Length 495;  
Best Local Similarity 77.8%; Pred. No. 40;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
||| ||||

Db 152 FYKLDIVPI 160

RESULT 32  
US-09-646-028-50  
; Sequence 50, Application US/09646028  
; Patent No. 6562347  
; GENERAL INFORMATION:  
; APPLICANT: Kwak, Larry  
; APPLICANT: Biragyn, Arya  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF  
; FILE REFERENCE: 14014.0316/P  
; CURRENT APPLICATION NUMBER: US/09/646,028  
; CURRENT FILING DATE: 2000-09-12  
; PRIOR APPLICATION NUMBER: 60/077,745  
; PRIOR FILING DATE: 1998-03-12  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 50  
; LENGTH: 587  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct  
US-09-646-028-50

Query Match 77.8%; Score 35; DB 4; Length 587;  
Best Local Similarity 77.8%; Pred. No. 48;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
||| ||||  
Db 248 FYKLDIVPI 256

RESULT 33  
US-09-646-028-56  
; Sequence 56, Application US/09646028  
; Patent No. 6562347  
; GENERAL INFORMATION:  
; APPLICANT: Kwak, Larry  
; APPLICANT: Biragyn, Arya  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF  
; FILE REFERENCE: 14014.0316/P  
; CURRENT APPLICATION NUMBER: US/09/646,028  
; CURRENT FILING DATE: 2000-09-12  
; PRIOR APPLICATION NUMBER: 60/077,745  
; PRIOR FILING DATE: 1998-03-12  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 56  
; LENGTH: 595  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct  
US-09-646-028-56

Query Match 77.8%; Score 35; DB 4; Length 595;  
Best Local Similarity 77.8%; Pred. No. 49;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
||| ||||  
Db 256 FYKLDIVPI 264

RESULT 34  
US-09-646-028-52  
; Sequence 52, Application US/09646028  
; Patent No. 6562347

GENERAL INFORMATION:  
APPLICANT: Kwak, Larry  
APPLICANT: Birszyn, Atya  
TITLE OF INVENTION: CHEMOKINES-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES  
FILE REFERENCE: 14014.0316/P  
CURRENT APPLICATION NUMBER: US/09/646,028  
PRIOR FILING DATE: 2000-09-12  
PRIOR APPLICATION NUMBER: 60/077,745  
PRIOR FILING DATE: 1998-03-12  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 52  
LENGTH: 601  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct  
US-09-646-028-52

Query Match 77.8%; Score 35; DB 4; Length 601;  
Best Local Similarity 77.8%; Pred. No. 49;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
DB 262 FYKLDIVPI 270

RESULT 35  
US-08-375-510-2  
Sequence 2, Application US/08375510  
Patent No. 5576421  
GENERAL INFORMATION:  
APPLICANT: Saito, Atsushi  
APPLICANT: Sinagawa, Hideo  
APPLICANT: Nakata, Atsuo  
TITLE OF INVENTION: HIV ANTIGEN  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolasch and Birch  
STREET: P.O. Box 747  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/375,510  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/985,949  
FILING DATE: 04-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Svensson, Leonard R.  
REGISTRATION NUMBER: 30,330  
REFERENCE/DOCKET NUMBER: 216-309P  
TELEPHONE: (703) 241-1300  
TELEFAX: (703) 241-2848  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 826 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-487-657-2

Query Match 77.8%; Score 35; DB 2; Length 826;  
Best Local Similarity 77.8%; Pred. No. 69;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
DB 148 FYKLDIVPI 156

RESULT 37

GENERAL INFORMATION:  
APPLICANT: Kwak, Larry  
APPLICANT: Birszyn, Atya  
TITLE OF INVENTION: CHEMOKINES-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES  
FILE REFERENCE: 14014.0316/P  
CURRENT APPLICATION NUMBER: US/09/646,028  
PRIOR FILING DATE: 2000-09-12  
PRIOR APPLICATION NUMBER: 60/077,745  
PRIOR FILING DATE: 1998-03-12  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 52  
LENGTH: 601  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct  
US-09-646-028-52

Query Match 77.8%; Score 35; DB 1; Length 826;  
Best Local Similarity 77.8%; Pred. No. 69;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
DB 148 FYKLDIVPI 156

RESULT 36  
US-08-487-657-2  
Sequence 2, Application US/08487657  
Patent No. 5834267  
GENERAL INFORMATION:  
APPLICANT: Saito, Atsushi  
APPLICANT: Sinagawa, Hideo  
APPLICANT: Nakata, Atsuo  
TITLE OF INVENTION: HIV ANTIGEN  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolasch and Birch  
STREET: P.O. Box 747  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,657  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/375,510  
FILING DATE: 18-JAN-1995  
APPLICATION NUMBER: US/07/985,949  
FILING DATE: 04-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Svensson, Leonard R.  
REGISTRATION NUMBER: 30,330  
REFERENCE/DOCKET NUMBER: 216-309P  
TELEPHONE: (703) 241-1300  
TELEFAX: (703) 241-2848  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 826 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-487-657-2

Query Match 77.8%; Score 35; DB 2; Length 826;  
Best Local Similarity 77.8%; Pred. No. 69;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
DB 148 FYKLDIVPI 156

RESULT 37

US-09-309-572-23  
; Sequence 23, Application US/09309572  
; Patent No. 6440730  
; GENERAL INFORMATION:  
; APPLICANT: Heinrich-Pette-Institut  
; TITLE OF INVENTION: Retroviral hybrid vectors pseudotyped with LCMV  
; FILE REFERENCE: P50489  
; CURRENT APPLICATION NUMBER: US/09/309,572  
; CURRENT FILING DATE: 1999-05-11  
; EARLIER APPLICATION NUMBER: DE 198 56 463  
; EARLIER FILING DATE: 1998-11-26  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 854  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
; FEATURE:  
; OTHER INFORMATION: envelope polyprotein  
US-09-309-572-23  
Query Match 77.8%; Score 35; DB 4; Length 854;  
Best Local Similarity 77.8%; Pred. No. 71;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 FYSLKIVPI 9  
Db 176 FYKLDIVPI 184  
RESULT 38  
US-09-718-096-23  
; Sequence 23, Application US/09718096  
; Patent No. 6589763  
; GENERAL INFORMATION:  
; APPLICANT: Von Laer, Meike-Dorothee  
; TITLE OF INVENTION: RETROVIRAL HYBRID VECTORS PSEUDOTYPED WITH LCMV  
; FILE REFERENCE: 35-195  
; CURRENT APPLICATION NUMBER: US/09/718,096  
; CURRENT FILING DATE: 2000-11-22  
; PRIOR APPLICATION NUMBER: DE 19856463.5  
; PRIOR FILING DATE: 1998-11-26  
; PRIOR APPLICATION NUMBER: EP 99250415.9  
; PRIOR FILING DATE: 1999-11-25  
; PRIOR APPLICATION NUMBER: US 09/309,572  
; PRIOR FILING DATE: 1999-05-11  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 854  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
; FEATURE:  
; OTHER INFORMATION: envelope polyprotein  
US-09-718-096-23  
Query Match 77.8%; Score 35; DB 4; Length 854;  
Best Local Similarity 77.8%; Pred. No. 71;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 FYSLKIVPI 9  
Db 176 FYKLDIVPI 184  
RESULT 39  
US-08-493-235-13  
; Sequence 13, Application US/08493235  
; Patent No. 5840313  
; GENERAL INFORMATION:  
; APPLICANT: Vahne, Anders  
; APPLICANT: Svennerholm, Bo  
; APPLICANT: Rymo, Lars

APPLICANT: Jeansson, Stig  
APPLICANT: Horal, Peter  
TITLE OF INVENTION: PEPTIDES FOR USE IN VACCINATION AND  
INDUCTION OF NEUTRALIZING ANTIBODIES AGAINST HUMAN  
TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR  
STREET: 620 NEWPORT CENTER DRIVE 16TH FLOOR  
CITY: NEWPORT BEACH  
STATE: CA  
COUNTRY: USA  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/493,235  
FILING DATE: 20 June 1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Kaiser, AnneMarie  
REGISTRATION NUMBER: 37,649  
REFERENCE/DOCKET NUMBER: METRICS.12CPC1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-235-8550  
TELEFAX: 619-235-0176  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
US-08-493-235-13  
Query Match 75.6%; Score 34; DB 2; Length 28;  
Best Local Similarity 66.7%; Pred. No. 3;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 FYSLKIVPI 9  
Db 12 FYKLDIVPI 20  
RESULT 40  
US-10-038-407-6  
; Sequence 6, Application US/10038407  
; Patent No. 6815201  
; GENERAL INFORMATION:  
; APPLICANT: Pinter, Abraham  
; TITLE OF INVENTION: HIV-1 gp120 V1/V2 DOMAIN EPITOPES  
; TITLE OF INVENTION: CAPABLE OF GENERATING NEUTRALIZING ANTIBODIES  
; FILE REFERENCE: 07763-048001  
; CURRENT APPLICATION NUMBER: US/10/038,407  
; CURRENT FILING DATE: 2002-01-02  
; PRIOR APPLICATION NUMBER: 09/508,208  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: PCT/US98/18679  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: 60/058,155  
; PRIOR FILING DATE: 1997-09-08  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus (HIV)

US-10-038-407-6

Query Match 75.6%; Score 34; DB 4; Length 28;  
Best Local Similarity 66.7%; Pred. No. 3;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 FYSLKIVPI 9  
Db 19 FYKLDVPI 27

Search completed: February 24, 2005, 19:16:10  
Job time : 43 secs

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OM protein - protein search, using sw model

Run on: February 24, 2005, 19:14:48 ; Search time 131 Seconds  
(without alignments)  
22.482 Million cell updates/sec

Title: US-09-914-205-5  
Perfect score: 45  
Sequence: 1 FVSLKIVPI 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
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3: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	91.1	765	US-10-437-963-112846	Sequence 112846,
2	38	84.4	485	US-10-866-527-48	Sequence 48, Appl
3	38	84.4	498	US-10-371-472-2	Sequence 2, Appl
4	38	84.4	498	US-10-371-472-5	Sequence 5, Appl
5	36	80.0	169	US-09-925-299-1125	Sequence 1125, Ap
6	36	80.0	169	US-09-925-299-1125	Sequence 1125, Ap
7	36	80.0	210	US-09-925-300-1354	Sequence 1354, Ap
8	36	80.0	453	US-09-935-642-8	Sequence 8, Appl
9	36	80.0	453	US-10-205-331-40	Sequence 40, Appl
10	36	80.0	453	US-10-408-765A-521	Sequence 521, App
11	36	80.0	453	US-10-408-765A-2214	Sequence 2214, Ap
12	36	80.0	453	US-10-408-765A-2215	Sequence 2215, Ap
13	36	80.0	469	US-10-371-472-23	Sequence 23, Appl

14	35	77.8	15	14	US-10-038-407-16	Sequence 16, Appl
15	35	77.8	34	14	US-10-038-407-2	Sequence 2, Appl
16	35	77.8	96	14	US-10-038-407-1	Sequence 1, Appl
17	35	77.8	245	15	US-10-282-122A-65500	Sequence 65500, A
18	35	77.8	278	15	US-10-264-237-1845	Sequence 1845, Ap
19	35	77.8	365	14	US-10-038-407-28	Sequence 28, Appl
20	35	77.8	468	17	US-10-866-527-24	Sequence 24, Appl
21	35	77.8	484	17	US-10-866-527-2	Sequence 2, Appl
22	35	77.8	486	17	US-10-866-527-102	Sequence 102, App
23	35	77.8	488	17	US-10-866-527-72	Sequence 72, Appl
24	35	77.8	490	17	US-10-866-527-56	Sequence 56, Appl
25	35	77.8	494	15	US-10-371-472-19	Sequence 19, Appl
26	35	77.8	495	15	US-10-371-472-25	Sequence 25, Appl
27	35	77.8	495	15	US-10-371-472-28	Sequence 28, Appl
28	35	77.8	503	9	US-09-753-841-4	Sequence 4, Appl
29	35	77.8	509	17	US-10-866-527-114	Sequence 114, App
30	35	77.8	511	17	US-10-866-527-94	Sequence 94, Appl
31	35	77.8	515	16	US-10-462-040A-49	Sequence 49, Appl
32	35	77.8	518	16	US-10-462-040A-45	Sequence 45, Appl
33	35	77.8	518	16	US-10-462-040A-46	Sequence 46, Appl
34	35	77.8	518	16	US-10-462-040A-47	Sequence 47, Appl
35	35	77.8	518	16	US-10-462-040A-48	Sequence 48, Appl
36	35	77.8	587	14	US-10-335-394-50	Sequence 50, Appl
37	35	77.8	595	14	US-10-335-394-56	Sequence 56, Appl
38	35	77.8	601	14	US-10-335-394-52	Sequence 52, Appl
39	35	77.8	795	9	US-09-254-783A-1	Sequence 1, Appl
40	35	77.8	795	13	US-10-152-058-1	Sequence 1, Appl
41	34	75.6	20	9	US-09-775-805-63	Sequence 63, Appl
42	34	75.6	20	16	US-10-753-339-63	Sequence 63, Appl
43	34	75.6	28	14	US-10-038-407-6	Sequence 6, Appl
44	34	75.6	30	9	US-09-775-805-23	Sequence 23, Appl
45	34	75.6	30	16	US-10-753-339-23	Sequence 23, Appl

## ALIGNMENTS

RESULT 1  
US-10-437-963-112846  
; Sequence 112846, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 112846  
; LENGTH: 765  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_16692C.1.pap  
US-10-437-963-112846

Query Match 91.1% Score 41; DB 16; Length 765;  
Best Local Similarity 77.8%; Pred No. 14;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FVSLKIVPI 9  
Db 99 FVSLKILPV 107

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RESULT 2
US-10-866-527-48
; Sequence 48, Application US/10866527
; Publication No. US20050025779A1
; GENERAL INFORMATION:
; APPLICANT: VaxGen, Inc.
; APPLICANT: Berman, Phillip W
; APPLICANT: Jobs, David V
; TITLE OF INVENTION: HIV-1 ENVELOPE GLYCOPROTEINS HAVING UNUSUAL DISULFIDE STRUCTURE
; FILE REFERENCE: 409J-000210US
; CURRENT APPLICATION NUMBER: US/10/866,527
; CURRENT FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-866-527-48
Query Match      84.4%; Score 38; DB 17; Length 485;
Best Local Similarity 77.8%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
Db      152 FYSLDVVP 160

RESULT 3
US-10-371-472-2
; Sequence 2, Application US/10371472
; Publication No. US20040052821A1
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/10/371,472
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US/09/419,362
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 498
; TYPE: PRT
; ORGANISM: HIV
US-10-371-472-2
Query Match      84.4%; Score 38; DB 15; Length 498;
Best Local Similarity 77.8%; Pred. No. 36;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 FYSLKIVPI 9
Db      156 FYSLDVVP 164

RESULT 4
US-10-371-472-5
; Sequence 5, Application US/10371472
; Publication No. US20040052821A1
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/10/371,472
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US/09/419,362
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 498
; TYPE: PRT
; ORGANISM: HIV
US-10-371-472-5
Query Match      84.4%; Score 38; DB 15; Length 498;
Best Local Similarity 77.8%; Pred. No. 36;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 FYSLKIVPI 9
Db      156 FYSLDVVP 164

RESULT 5
US-09-925-299-1125
; Sequence 1125, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1125
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-1125
Query Match      80.0%; Score 36; DB 9; Length 169;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 FYSLKIVP 8
Db      14 FYSLKVP 21

RESULT 6
US-09-925-299-1125
; Sequence 1125, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
US-09-925-299-1125
Query Match      80.0%; Score 36; DB 9; Length 169;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 FYSLKIVP 8
Db      14 FYSLKVP 21
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; SEQ ID NO 1125
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-1125

Query Match      80.0%; Score 36; DB 10; Length 169;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKVP 8
Db 14 FYSLKVP 21

RESULT 7
US-09-925-300-1354
; Sequence 1354, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1354
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (192)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (208)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1354

Query Match      80.0%; Score 36; DB 9; Length 210;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKVP 8
Db 14 FYSLKVP 21

RESULT 8
US-09-935-642-8
; Sequence 8, Application US/09935642
; Publication No. US20030044795A1
; GENERAL INFORMATION:
; APPLICANT: BYRJALSEN, Inger
; APPLICANT: LARSEN, Peter
; APPLICANT: STEPHEN, John
; TITLE OF INVENTION: Biochemical Markers for the Human
; TITLE OF INVENTION: Endometrium
; FILE REFERENCE: 8969-014
; CURRENT APPLICATION NUMBER: US/09/935,642
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: PCT/GB97/02394
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: PCT/GB9707132.8
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: PCT/GB9618600.2
; PRIOR FILING DATE: 1996-09-06
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; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-642-8

Query Match      80.0%; Score 36; DB 10; Length 453;
Best Local Similarity 75.0%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKVP 8
Db 13 FYSLKVP 20

RESULT 9
US-10-205-331-40
; Sequence 40, Application US/10205331
; Publication No. US20040058326A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Finnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018199
; CURRENT APPLICATION NUMBER: US/10/205,331
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Core protein II of human mitochondrial cytochrome bc-1 complex
US-10-205-331-40

Query Match      80.0%; Score 36; DB 15; Length 453;
Best Local Similarity 75.0%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKVP 8
Db 13 FYSLKVP 20

RESULT 10
US-10-408-765A-521
; Sequence 521, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 521
; LENGTH: 453
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-521

Query Match      80.0%; Score 36; DB 16; Length 453;
Best Local Similarity 75.0%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVP 8
Db 13 FYSLKVP 20

RESULT 11
US-10-408-765A-2214
; Sequence 2214, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT FILING DATE: 2003-04-04
; CURRENT APPLICATION NUMBER: US/10/408,765A
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2214
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2214

Query Match      80.0%; Score 36; DB 16; Length 453;
Best Local Similarity 75.0%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVP 8
Db 13 FYSLKVP 20

RESULT 12
US-10-408-765A-2215
; Sequence 2215, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT FILING DATE: 2003-04-04
; CURRENT APPLICATION NUMBER: US/10/408,765A
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2215
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2215

Query Match      80.0%; Score 36; DB 16; Length 453;
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Best Local Similarity 75.0%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVP 8
Db 13 FYSLKVP 20

RESULT 13
US-10-371-472-23
; Sequence 23, Application US/10371472
; Publication No. US20040052821A1
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/10/371,472
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US/09/419,362
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 469
; TYPE: PRT
; ORGANISM: HIV
US-10-371-472-23

Query Match      80.0%; Score 36; DB 15; Length 469;
Best Local Similarity 77.8%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
Db 140 FYKLNIVPI 148

RESULT 14
US-10-038-407-16
; Sequence 16, Application US/10038407
; Publication No. US20030105282A1
; GENERAL INFORMATION:
; APPLICANT: Pinter, Abraham
; TITLE OF INVENTION: HIV-1 gp120 V1/V2 DOMAIN EPITOPES
; FILE REFERENCE: 07763-048001
; CURRENT APPLICATION NUMBER: US/10/038,407
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: 09/508,208
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US98/186679
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/058,155
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus (HIV)
US-10-038-407-16

Query Match      77.8%; Score 35; DB 14; Length 15;
Best Local Similarity 77.8%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
Db 5 FYKLDIVPI 13
```

```
RESULT 15
US-10-038-407-2
; Sequence 2, Application US/10038407
; Publication NO. US20030105282A1
; GENERAL INFORMATION:
; APPLICANT: Pinter, Abraham
; TITLE OF INVENTION: HIV-1 gp120 V1/V2 DOMAIN EPITOPES
; FILE REFERENCE: 07763-048001
; CURRENT APPLICATION NUMBER: US/10/038,407
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: 09/508,208
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US98/18679
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/058,155
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus (HIV)
US-10-038-407-2
Query Match      77.8%; Score 35; DB 14; Length 34;
Best Local Similarity 77.8%; Pred. No. 8.8;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
      ||| |||||
DB      25 FYKLDIVPI 33

RESULT 16
US-10-038-407-1
; Sequence 1, Application US/10038407
; Publication NO. US20030105282A1
; GENERAL INFORMATION:
; APPLICANT: Pinter, Abraham
; TITLE OF INVENTION: CAPABLE OF GENERATING NEUTRALIZING ANTIBODIES
; FILE REFERENCE: 07763-048001
; CURRENT APPLICATION NUMBER: US/10/038,407
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: 09/508,208
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US98/18679
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/058,155
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus (HIV)
US-10-038-407-1
Query Match      77.8%; Score 35; DB 14; Length 96;
Best Local Similarity 77.8%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
      ||| |||||
DB      66 FYKLDIVPI 74

RESULT 17
US-10-282-122A-65500
; Sequence 65500, Application US/10282122A
```

```
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65500
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-282-122A-65500
Query Match      77.8%; Score 35; DB 15; Length 245;
Best Local Similarity 55.6%; Pred. No. 69;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
      ||| |||||
DB      179 FYSFKLLPV 187

RESULT 18
US-10-264-237-1845
; Sequence 1845, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131PI
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1845
```

```
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (234)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (244)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC FEATURE
; LOCATION: (247)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (262)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-1845
```

```
Query Match 77.8%; Score 35; DB 15; Length 278;
Best Local Similarity 62.5%; Pred. No. 79;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 YSLKIVPI 9
Db 197 YSIKVVPI 204
```

```
RESULT 19
US-10-038-407-28
; Sequence 28, Application US/10038407
; Publication No. US20030105282A1
; GENERAL INFORMATION:
; APPLICANT: Pinter, Abraham
; TITLE OF INVENTION: HIV-1 gp120 V1/V2 DOMAIN EPITOPES
; FILE REFERENCE: 07763-048001
; CURRENT APPLICATION NUMBER: US/10/038,407
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: 09/508,208
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US98/18679
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/058,155
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus (HIV)
US-10-038-407-28
```

```
Query Match 77.8%; Score 35; DB 14; Length 365;
Best Local Similarity 77.8%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 FYSLKIVPI 9
Db 335 FYKLDIVPI 343
```

```
RESULT 20
US-10-866-527-24
; Sequence 24, Application US/10866527
; Publication No. US20050025779A1
; GENERAL INFORMATION:
; APPLICANT: VaxGen, Inc.
; APPLICANT: Berman, Phillip W
; APPLICANT: Jobs, David V
; TITLE OF INVENTION: HIV-1 ENVELOPE GLYCOPROTEINS HAVING UNUSUAL DISULFIDE STRUCTURE
```

```
; FILE REFERENCE: 409J-000210US
; CURRENT APPLICATION NUMBER: US/10/866,527
; CURRENT FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-866-527-24
```

```
Query Match 77.8%; Score 35; DB 17; Length 468;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 FYSLKIVPI 9
Db 141 FYALDVPI 149
```

```
RESULT 21
US-10-866-527-2
; Sequence 2, Application US/10866527
; Publication No. US20050025779A1
; GENERAL INFORMATION:
; APPLICANT: VaxGen, Inc.
; APPLICANT: Berman, Phillip W
; APPLICANT: Jobs, David V
; TITLE OF INVENTION: HIV-1 ENVELOPE GLYCOPROTEINS HAVING UNUSUAL DISULFIDE STRUCTURE
; FILE REFERENCE: 409J-000210US
; CURRENT APPLICATION NUMBER: US/10/866,527
; CURRENT FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-866-527-2
```

```
Query Match 77.8%; Score 35; DB 17; Length 484;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 FYSLKIVPI 9
Db 152 FYKLDIVPI 160
```

```
RESULT 22
US-10-866-527-102
; Sequence 102, Application US/10866527
; Publication No. US20050025779A1
; GENERAL INFORMATION:
; APPLICANT: VaxGen, Inc.
; APPLICANT: Berman, Phillip W
; APPLICANT: Jobs, David V
; TITLE OF INVENTION: HIV-1 ENVELOPE GLYCOPROTEINS HAVING UNUSUAL DISULFIDE STRUCTURE
; FILE REFERENCE: 409J-000210US
; CURRENT APPLICATION NUMBER: US/10/866,527
; CURRENT FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 102
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-866-527-102
```

```
Query Match 77.8%; Score 35; DB 17; Length 486;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 FYSLKIVPI 9
Db      155 FYKLDIVPI 163

RESULT 23
US-10-866-527-72
; Sequence 72, Application US/10866527
; Publication No. US20050025779A1
; GENERAL INFORMATION:
; APPLICANT: VaxGen, Inc.
; APPLICANT: Berman, Phillip W
; APPLICANT: Jobs, David V
; TITLE OF INVENTION: HIV-1 ENVELOPE GLYCOPROTEINS HAVING UNUSUAL DISULFIDE STRUCTURE
; FILE REFERENCE: 4093-000210US
; CURRENT APPLICATION NUMBER: US/10/866,527
; CURRENT FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-866-527-72

Query Match      77.8%; Score 35; DB 17; Length 488;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
Db      147 FYKLDIVPI 155

RESULT 24
US-10-866-527-56
; Sequence 56, Application US/10866527
; Publication No. US20050025779A1
; GENERAL INFORMATION:
; APPLICANT: VaxGen, Inc.
; APPLICANT: Berman, Phillip W
; APPLICANT: Jobs, David V
; TITLE OF INVENTION: HIV-1 ENVELOPE GLYCOPROTEINS HAVING UNUSUAL DISULFIDE STRUCTURE
; FILE REFERENCE: 4093-000210US
; CURRENT APPLICATION NUMBER: US/10/866,527
; CURRENT FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-866-527-56

Query Match      77.8%; Score 35; DB 17; Length 490;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
Db      151 FYKLDIVPI 159

RESULT 25
US-10-371-472-19
; Sequence 19, Application US/10371472
; Publication No. US20040052821A1
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/10/371,472
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 494
; TYPE: PRT
; ORGANISM: HIV
US-10-371-472-19

Query Match      77.8%; Score 35; DB 15; Length 494;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
Db      145 FYKLDIVPI 153

RESULT 26
US-10-371-472-25
; Sequence 25, Application US/10371472
; Publication No. US20040052821A1
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/10/371,472
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US/09/419,362
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 495
; TYPE: PRT
; ORGANISM: HIV
US-10-371-472-25

Query Match      77.8%; Score 35; DB 15; Length 495;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
Db      152 FYKLDIVPI 160

RESULT 27
US-10-371-472-28
; Sequence 28, Application US/10371472
; Publication No. US20040052821A1
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/10/371,472
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US/09/419,362
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 496
; TYPE: PRT
; ORGANISM: HIV
US-10-371-472-28

Query Match      77.8%; Score 35; DB 15; Length 496;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 28  
; LENGTH: 495  
; TYPE: PRT  
; ORGANISM: HIV  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(495)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-10-371-472-28

Query Match 77.8%; Score 35; DB 15; Length 495;  
Best Local Similarity 77.8%; Pred. No. 1.4e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
DB 152 FYKLDIVPI 160

RESULT 28  
US-09-759-841-4  
; Sequence 4, Application US/09759841  
; Patent No. US20010039026A1  
; GENERAL INFORMATION:  
; APPLICANT: Rickett, Graham A  
; APPLICANT: Dobbs, Susan  
; APPLICANT: Perros, Manousos  
; TITLE OF INVENTION: Assay Method  
; FILE REFERENCE: PC10348APME  
; CURRENT APPLICATION NUMBER: US/09/759,841  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: GB 0000661.9  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: GB 0000663.5  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: GB 0000659.3  
; PRIOR FILING DATE: 2000-01-12  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 503  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-759-841-4

Query Match 77.8%; Score 35; DB 9; Length 503;  
Best Local Similarity 77.8%; Pred. No. 1.5e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
DB 173 FYELDIVPI 181

RESULT 29  
US-10-866-527-114  
; Sequence 114, Application US/10866527  
; Publication No. US20050025779A1  
; GENERAL INFORMATION:  
; APPLICANT: VaxGen, Inc.  
; APPLICANT: Berman, Phillip W  
; APPLICANT: Jones, David V  
; TITLE OF INVENTION: HIV-1 ENVELOPE GLYCOPROTEINS HAVING UNUSUAL DISULFIDE STRUCTURE  
; FILE REFERENCE: 409J-000210US  
; CURRENT APPLICATION NUMBER: US/10/866,527  
; CURRENT FILING DATE: 2004-06-10  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 114  
; LENGTH: 509  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1

US-10-866-527-114

Query Match 77.8%; Score 35; DB 17; Length 509;  
Best Local Similarity 77.8%; Pred. No. 1.5e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
DB 151 FYKLDIVPI 159

RESULT 30  
US-10-866-527-94  
; Sequence 94, Application US/10866527  
; Publication No. US20050025779A1  
; GENERAL INFORMATION:  
; APPLICANT: VaxGen, Inc.  
; APPLICANT: Berman, Phillip W  
; APPLICANT: Jones, David V  
; TITLE OF INVENTION: HIV-1 ENVELOPE GLYCOPROTEINS HAVING UNUSUAL DISULFIDE STRUCTURE  
; FILE REFERENCE: 409J-000210US  
; CURRENT APPLICATION NUMBER: US/10/866,527  
; CURRENT FILING DATE: 2004-06-10  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 94  
; LENGTH: 511  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-10-866-527-94

Query Match 77.8%; Score 35; DB 17; Length 511;  
Best Local Similarity 77.8%; Pred. No. 1.5e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
DB 152 FYKLDIVPI 160

RESULT 31  
US-10-462-040A-49  
; Sequence 49, Application US/10462040A  
; Publication No. US20040106105A1  
; GENERAL INFORMATION:  
; APPLICANT: TORAN GARCIA, JOSE LUIS  
; APPLICANT: MARTINEZ ALONSO, CARLOS  
; TITLE OF INVENTION: VACCINE  
; FILE REFERENCE: 621032-8/JP/B-5129  
; CURRENT APPLICATION NUMBER: US/10/462,040A  
; CURRENT FILING DATE: 2003-06-12  
; PRIOR APPLICATION NUMBER: EP 02380126.9  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 49  
; LENGTH: 515  
; TYPE: PRT  
; ORGANISM: Human Immunodeficiency Virus type 1  
US-10-462-040A-49

Query Match 77.8%; Score 35; DB 16; Length 515;  
Best Local Similarity 77.8%; Pred. No. 1.5e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
DB 184 FYKLDIVPI 192

RESULT 32  
US-10-462-040A-45  
; Sequence 45, Application US/10462040A



```
; Publication NO. US20040106105A1
; GENERAL INFORMATION:
; APPLICANT: TORAN GARCIA, JOSE LUIS
; APPLICANT: MARTINEZ ALONSO, CARLOS
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: 621032-8/JP/B-5129
; CURRENT APPLICATION NUMBER: US/10/462,040A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: EP 02380126.9
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus type 1
US-10-462-040A-45

Query Match      77.8%; Score 35; DB 16; Length 518;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
Db 184 FVKLDIVPI 192

RESULT 33
US-10-462-040A-46
; Sequence 46, Application US/10462040A
; Publication No. US20040106105A1
; GENERAL INFORMATION:
; APPLICANT: TORAN GARCIA, JOSE LUIS
; APPLICANT: MARTINEZ ALONSO, CARLOS
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: 621032-8/JP/B-5129
; CURRENT APPLICATION NUMBER: US/10/462,040A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: EP 02380126.9
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus type 1
US-10-462-040A-46

Query Match      77.8%; Score 35; DB 16; Length 518;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
Db 184 FVKLDIVPI 192

RESULT 34
US-10-462-040A-47
; Sequence 47, Application US/10462040A
; Publication No. US20040106105A1
; GENERAL INFORMATION:
; APPLICANT: TORAN GARCIA, JOSE LUIS
; APPLICANT: MARTINEZ ALONSO, CARLOS
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: 621032-8/JP/B-5129
; CURRENT APPLICATION NUMBER: US/10/462,040A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: EP 02380126.9
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47

Query Match      77.8%; Score 35; DB 16; Length 518;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
Db 184 FVKLDIVPI 192

RESULT 35
US-10-462-040A-48
; Sequence 48, Application US/10462040A
; Publication No. US20040106105A1
; GENERAL INFORMATION:
; APPLICANT: TORAN GARCIA, JOSE LUIS
; APPLICANT: MARTINEZ ALONSO, CARLOS
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: 621032-8/JP/B-5129
; CURRENT APPLICATION NUMBER: US/10/462,040A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: EP 02380126.9
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus type 1
US-10-462-040A-48

Query Match      77.8%; Score 35; DB 16; Length 518;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
Db 184 FVKLDIVPI 192

RESULT 36
US-10-335-394-50
; Sequence 50, Application US/10335394
; Publication No. US20030138452A1
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/10/335,394
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 50
; LENGTH: 587
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-10-335-394-50

Query Match      77.8%; Score 35; DB 14; Length 587;
Best Local Similarity 77.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 FYSLKIVPI 9
Db      248 FYKLDIVPI 256

RESULT 37
US-10-335-394-56
; Sequence 56, Application US/10335394
; Publication No. US20030138452A1
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/10/335,394
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-10-335-394-56

Query Match      77.8%; Score 35; DB 14; Length 595;
Best Local Similarity 77.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
Db      256 FYKLDIVPI 264

RESULT 38
US-10-335-394-52
; Sequence 52, Application US/10335394
; Publication No. US20030138452A1
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/10/335,394
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 601
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-10-335-394-52

Query Match      77.8%; Score 35; DB 14; Length 601;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
Db      248 FYKLDIVPI 256

RESULT 39
US-09-254-783A-1
; Sequence 1, Application US/09254783A
; Patent No. US20020035734A1
; GENERAL INFORMATION:
; APPLICANT: Boeynaems, Jeanmarie
; APPLICANT: Communi, Didier
; TITLE OF INVENTION: G Protein Coupled Receptor Showing Selective Affinity for ATP
; FILE REFERENCE: 9409/2062
; CURRENT APPLICATION NUMBER: US/09/254,783A
; CURRENT FILING DATE: 1999-08-16
; PRIOR APPLICATION NUMBER: PCT/BE98/00108
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: EP97870101.9
; PRIOR FILING DATE: 1997-07-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 795
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-09-254-783A-1

Query Match      77.8%; Score 35; DB 9; Length 795;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 YSLKIVPI 9
Db      197 YSIKVPV 204

RESULT 40
US-10-152-058-1
; Sequence 1, Application US/10152058
; Publication No. US20020142988A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; APPLICANT: Boeynaems, Jeanmarie
; TITLE OF INVENTION: G Protein Coupled Receptor Showing Selective Affinity for ATP
; FILE REFERENCE: 9409/2062
; CURRENT APPLICATION NUMBER: US/10/152,058
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: PCT/BE98/00108
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: EP97870101.9
; PRIOR FILING DATE: 1997-07-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 795
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-10-152-058-1

Query Match      77.8%; Score 35; DB 13; Length 795;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 YSLKIVPI 9
Db      197 YSIKVPV 204

Search completed: February 24, 2005, 19:27:11
Job time : 132 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 24, 2005, 19:03:44 ; Search time 39 Seconds

(without alignments)  
22,204 Million cell updates/sec

Title: US-09-914-205-5

Perfect score: 45

Sequence: 1 FYSLKIVPI 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	82.2	301	2 T24651	hypothetical prote
2	37	82.2	383	2 AB2808	hypothetical prote
3	37	82.2	383	2 H97586	probable sulfonate
4	37	82.2	1000	2 F70368	cation efflux (Acr
5	36	80.0	115	2 T07576	hypothetical prote
6	36	80.0	253	2 D70166	pnp protein (pnp
7	36	80.0	452	1 S29510	ubiquinol-cytochro
8	36	80.0	453	1 A32629	ubiquinol-cytochro
9	36	80.0	453	1 ZPBOC2	ubiquinol-cytochro
10	36	80.0	2054	2 T07584	hypothetical prote
11	35	77.8	211	2 S25938	env protein - huma
12	35	77.8	219	2 S25939	env protein - huma
13	35	77.8	245	2 F81162	ubiquinone/menaqui
14	35	77.8	473	2 JC7359	splicing factor, S
15	35	77.8	506	2 A40218	envelope glycoprote
16	35	77.8	553	2 G90593	subtilisin, serine
17	35	77.8	843	1 H44001	env polypeptidase
18	35	77.8	846	1 VCLJND	env polypeptidase
19	35	77.8	852	1 VCLJBR	env polypeptidase
20	35	77.8	854	2 S13288	env protein - huma
21	34	75.6	218	2 G72754	probable phosphoen
22	34	75.6	526	2 D71805	protein-export mem
23	34	75.6	591	2 A99444	acylaminoacyl-pept
24	34	75.6	729	1 VCLJXJ	env polypeptidase
25	34	75.6	847	2 T09448	envelope glycoprot
26	34	75.6	847	2 S13289	env protein - huma
27	34	75.6	851	2 S33985	env polypeptidase
28	34	75.6	852	2 T12016	envelope glycoprot
29	34	75.6	853	2 S54384	envelope polypept

30 34 75.6 855 1 VCLJZR env polypeptidase  
31 34 75.6 856 1 A44963 env polypeptidase  
32 34 75.6 856 1 VCLJ3W env polypeptidase  
33 34 75.6 856 1 VCLJH3 env polypeptidase  
34 34 75.6 856 1 VCLJVL env polypeptidase  
35 34 75.6 861 1 VCLJSC env polypeptidase  
36 34 75.6 861 1 VCLJKB env polypeptidase  
37 34 75.6 861 1 VCLJLV env polypeptidase  
38 34 75.6 1882 1 GNVVTR genome polypeptidase  
39 33 73.3 82 2 T17870 hypothetical prote  
40 33 73.3 253 2 B87667 ABC-2 type transpo  
41 33 73.3 259 2 F82707 conserved hypothet  
42 33 73.3 347 2 T21067 hypothetical prote  
43 33 73.3 399 2 S54644 translation initia  
44 33 73.3 437 2 C72600 hypothetical prote  
45 33 73.3 454 2 H83773 transcription regu

## ALIGNMENTS

### RESULT 1

T24651

hypothetical protein T07C5.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T24651

R:McMurray, A.

submitted to the EMBL Data Library, July 1995

A:Reference number: Z19917

A:Accession: T24651

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-301 <WIL>

A:Cross-references: UNIPROT:Q22299; EMBL:Z50006; PIDN:CAA90300.1; GSPDB:GN00028; CESP:T07C5

A:Experimental source: clone T07C5

C:Genetics:

A:Gene: CESP:T07C5.4

A:Map position: X

A:Introns: 20/3; 223/1

Query Match 82.2%; Score 37; DB 2; Length 301;

Best Local Similarity 77.8%; Pred. No. 6.4;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9

Db 103 YYSTKIVPI 111

### RESULT 2

AB2808

hypothetical protein ssuA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C:Species: Agrobacterium tumefaciens

C>Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004

C:Accession: AB2808

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan

i Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E

ster, E.W.

A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; MUID:21608550; PMID:11743193

A:Accession: AB2808

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-383 <KUR>

A:Cross-references: UNIPROT:Q8UE77; GB:AE008688; PIDN:AAL42880.1; PID:g17740332; GSPDB:G

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: ssuA

A:Map position: circular chromosome

Query Match 82.2%; Score 37; DB 2; Length 383;  
Best Local Similarity 87.5%; Pred. No. 8.2;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVP 8  
|||:|  
Db 361 FYDLKIVP 368

RESULT 3  
H97586  
probable sulfonate binding protein precursor (AF075709) [imported] - Agrobacterium tumefaciens  
C:Species: Agrobacterium tumefaciens  
C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C:Accession: H97586  
A: Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ouello, B.; Goldman, A.; Li, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001  
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens  
A:Reference number: A97359; MUID:21608551; PMID:11743194  
A:Accession: H97586  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-383 <KUR>  
A:Cross-references: UNIPROT:Q8UE77; GB:AE007869; PIDN:AAK87649.1; PID:g15157002; GSPDB:C  
C:Genetics:  
A:Gene: AGR\_C\_3458  
A:Map position: circular chromosome

Query Match 82.2%; Score 37; DB 2; Length 383;  
Best Local Similarity 87.5%; Pred. No. 8.2;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVP 8  
|||:|  
Db 361 FYDLKIVP 368

RESULT 4  
F70368  
cation efflux (AcrB/AcrD/AcrF family) - Aquifex aeolicus  
C:Species: Aquifex aeolicus  
C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
C:Accession: F70368  
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.  
Nature 392, 353-358, 1998  
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A:Reference number: A70300; MUID:98196866; PMID:9537320  
A:Accession: F70368  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1000 <AQF>  
A:Cross-references: UNIPROT:Q66977; GB:AE000707; NID:G2983342; PIDN:AAC06934.1; PID:g2983342  
A:Experimental source: strain VF5  
C:Genetics:  
A:Gene: acrB4  
C:Superfamily: acriflavin resistance protein

Query Match 82.2%; Score 37; DB 2; Length 1000;  
Best Local Similarity 87.5%; Pred. No. 21;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSLKIVPI 9  
|||:|  
Db 25 YSLKIVPI 32

RESULT 5  
T07576  
hypothetical protein 115 - Japanese black pine chloroplast  
C:Species: chloroplast Pinus thunbergiana (Japanese black pine)

C:Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 09-Jul-2004  
C:Accession: T07576  
R:Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiyama, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994  
A:Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genome  
A:Reference number: Z16030; MUID:95024047; PMID:7937893  
A:Accession: T07576  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-115 <WAK>  
A:Cross-references: UNIPROT:Q33000; EMBL:D17510; NID:G529643; PIDN:BAA04452.1; PID:g1262;  
C:Genetics:  
A:Genome: chloroplast  
C:Keywords: chloroplast

Query Match 80.0%; Score 36; DB 2; Length 115;  
Best Local Similarity 66.7%; Pred. No. 4;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
|||:|  
Db 7 FYSIKLPPI 15

RESULT 6  
D70166  
pHNP protein (phnP) homolog - Lyme disease spirochete  
C:Species: Borrelia burgdorferi (Lyme disease spirochete)  
C:Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 09-Jul-2004  
C:Accession: D70166  
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lachigra, R.; White, son, D.; Peterson, J.; Kervage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997  
A:Authors: Smith, H.O.; Venter, J.C.  
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.  
A:Reference number: A70100; MUID:98065943; PMID:9403685  
A:Accession: D70166  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-253 <KLE>  
A:Cross-references: UNIPROT:O51483; GB:AE001155; GB:AE000783; NID:G2688448; PIDN:AAC6690;  
A:Experimental source: strain E31  
C:Superfamily: ATP-binding protein PhnP (PhnP)

Query Match 80.0%; Score 36; DB 2; Length 253;  
Best Local Similarity 88.9%; Pred. No. 8.8;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
|||:|  
Db 141 FKSLKIVPI 149

RESULT 7  
S29510  
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) core protein II precursor - rat  
N:Alternate names: cytochrome bcl complex core protein II  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 07-May-1993 #sequence\_revision 14-Jul-1994 #text\_change 09-Jul-2004  
C:Accession: S29510  
R:Hosokawa, Y.; Suzuki, H.; Toda, H.; Nishikimi, M.; Ozawa, T. Biochem. Int. 20, 731-737, 1990  
A:Title: The primary structure of the precursor to core protein II, a putative member of ce analysis.  
A:Reference number: S29510; MUID:90282728; PMID:2162168  
A:Accession: S29510  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-452 <HOS>  
A:Cross-references: UNIPROT:P32551  
C:Genetics:  
A:Genome: nuclear

C:Superfamily: mitochondrial processing peptidase alpha chain  
C:Keywords: mitochondrial matrix; mitochondrion; oxidative phosphorylation; oxidoreducta  
F:1-14/Domain: transit peptide (mitochondrion) #status predicted <TNP>  
F:15-452/Product: ubiquinol-cytochrome-c reductase core protein II #status predicted <MA

Query Match 80.0%; Score 36; DB 1; Length 452;  
Best Local Similarity 75.0%; Pred. No. 16;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVP 8  
Db 13 FYSLKVAP 20

RESULT 8  
T07584  
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) core protein II precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 21-May-1990 #sequence\_revision 14-Jul-1994 #text\_change 09-Jul-2004  
C:Accession: A32629  
R:Hosokawa, Y.; Suzuki, H.; Toda, H.; Nishikimi, M.; Ozawa, T.  
J. Biol. Chem. 264, 13483-13488, 1989  
A:Title: Complementary DNA encoding core protein II of human mitochondrial cytochrome b  
A:Reference number: A32629; MUID:89340421; PMID:2547763  
A:Accession: A32629  
A:Molecule type: mRNA  
A:Residues: 1-453 <HOS>  
A:Cross-references: UNIPROT:P22695; GB:J04973; NID:G180927; PIDN:AAA35710.1; PID:G180928  
A:Note: the authors translated the codon AGA for residue 360 as Thr  
C:Genetics:  
A:Gene: GDB:UQCRC2  
A:Cross-references: GDB:141851; OMIM:191329  
A:Map position: 16p12.3-16p12.3  
C:Superfamily: mitochondrial processing peptidase alpha chain  
C:Keywords: hydrolase; mitochondrial matrix; mitochondrion; oxidative phosphorylation; o  
F:1-14/Domain: transit peptide (mitochondrion) #status predicted <TNP>  
F:15-453/Product: ubiquinol-cytochrome-c reductase core protein II #status predicted <MA

Query Match 80.0%; Score 36; DB 1; Length 453;  
Best Local Similarity 75.0%; Pred. No. 16;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVP 8  
Db 13 FYSLKVAP 20

RESULT 9  
ZFEOC2  
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) core protein II precursor - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 09-Jul-2004  
C:Accession: S16221; S14093  
R:Gencic, S.; Schaeffer, H.; von Jagow, G.  
Eur. J. Biochem. 199, 123-131, 1991  
A:Title: Core I protein of bovine ubiquinol-cytochrome-c reductase; an additional member  
of the proteins.  
A:Reference number: S16220; MUID:91293112; PMID:1712295  
A:Accession: S16221  
A:Molecule type: mRNA  
A:Residues: 1-453 <GEN>  
A:Cross-references: UNIPROT:P23004; GB:X59693; NID:G299; PIDN:CAA42214.1; PID:G300  
A:Note: part of this sequence, including the amino end of the mature protein, was confir  
R:Cocco, T.; Lorusso, M.; Sardanelli, A.M.; Minuto, M.; Ronchi, S.; Tedeschi, G.; Papa,  
Eur. J. Biochem. 195, 731-734, 1991  
A:Title: Structural and functional characteristics of polypeptide subunits of the bovine  
A:Reference number: S14093; MUID:91153313; PMID:1847870  
A:Accession: S14093  
A:Molecule type: protein  
A:Residues: 'T', 16-40, 'R', 42-46 <COC>  
C:Superfamily: mitochondrial processing peptidase alpha chain  
C:Keywords: hydrolase; mitochondrial matrix; mitochondrion; oxidative phosphorylation; c  
F:1-14/Domain: transit peptide (mitochondrion) #status predicted <TNP>

F:15-453/Product: ubiquinol-cytochrome-c reductase core protein II #status experimental <  
C:Superfamily: mitochondrial processing peptidase alpha chain  
C:Keywords: mitochondrial matrix; mitochondrion; oxidative phosphorylation; oxidoreducta  
F:1-14/Domain: transit peptide (mitochondrion) #status predicted <TNP>  
F:15-452/Product: ubiquinol-cytochrome-c reductase core protein II #status predicted <MA

Query Match 80.0%; Score 36; DB 1; Length 453;  
Best Local Similarity 75.0%; Pred. No. 16;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVP 8  
Db 13 FYSLKVAP 20

RESULT 10  
T07584  
hypochemical protein 2054 - Japanese black pine chloroplast  
C:Species: chloroplast Pinus thunbergiana (Japanese black pine)  
C:Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 09-Jul-2004  
C:Accession: T07584  
R:Wakasugi, T.; Teudzuki, J.; Ito, S.; Nakashima, K.; Teudzuki, T.; Sugiyura, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994  
A:Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genome  
A:Reference number: Z16030; MUID:95024047; PMID:7937893  
A:Accession: T07584  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-2054 <WAK>  
A:Cross-references: UNIPROT:P41653; EMBL:D17510; NID:G529643; PIDN:BAA04460.1; PID:G1262;  
C:Genetics:  
A:Genome: chloroplast  
C:Keywords: chloroplast

Query Match 80.0%; Score 36; DB 2; Length 2054;  
Best Local Similarity 66.7%; Pred. No. 70;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
Db 97 FYSLKIVPI 105

RESULT 11  
S25938  
env protein - human immunodeficiency virus type 1 (fragment)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 25-Feb-1994 #sequence\_revision 30-Jan-1998 #text\_change 09-Jul-2004  
C:Accession: S25938  
R:Guo, H.G.; Chermann, J.C.; Waters, D.; Hall, L.; Louie, A.; Gallo, R.C.; Streicher, H.;  
Nature 349, 745-746, 1991  
A:Title: Sequence analysis of original HIV-1.  
A:Reference number: S25937; MUID:91156044; PMID:2000145  
A:Accession: S25938  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-211 <GUO>  
A:Cross-references: UNIPROT:Q79141; EMBL:X57446; NID:G60204; PIDN:CAA40692.1; PID:G60205  
A:Experimental source: strain JBB  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1991  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: coat protein

Query Match 77.8%; Score 35; DB 2; Length 211;  
Best Local Similarity 77.8%; Pred. No. 12;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
Db 134 FYKLIVPI 142

RESULT 12  
S25939  
env protein - human immunodeficiency virus type 1 (fragment)

C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 25-Feb-1994 #sequence\_revision 30-Jan-1998 #text\_change 09-Jul-2004  
 C:Accession: S25939  
 R:Guo, H.G.; Chermann, J.C.; Waters, D.; Hall, L.; Louie, A.; Gallo, R.C.; Streicher, H.  
 Nature 349, 745-746, 1991  
 A:Title: Sequence analysis of original HIV-1.  
 A:Reference number: S25937; MUID:91156044; PMID:2000145  
 A:Accession: S25939  
 A:Molecule type: DNA  
 A:Residues: 1-219 <GUO>  
 A:Cross-references: UNIPROT:Q79144; EMBL:X57447; NID:G60212; PIDN:CAA406  
 A:Note: The nucleotide sequence was submitted to the EMBL Data Library, March 1991  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: Coat protein

Query Match 77.8%; Score 35; DB 2; Length 219;  
 Best Local Similarity 77.8%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
 ||| |||||  
 Db 134 FYKLDIVPI 142

RESULT 13  
 F81162  
 ubiquinone/menaquinone biosynthesis methyltransferase UbiE NMB0743 [imported] - Neisseria  
 C:Species: Neisseria meningitidis  
 C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
 C:Accession: F81162  
 R:Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
 Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.  
 Science 287, 1809-1815, 2000  
 A:Authors: Grand, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V  
 A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
 A:Reference number: A81000; MUID:20175755; PMID:10710307  
 A:Accession: F81162  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-245 <TET>  
 A:Cross-references: UNIPROT:Q9K075; GB:AE002429; GB:AE002098; NID:G7225969; PIDN:AAF4115  
 A:Experimental source: serogroup B, strain MC58  
 C:Genetics:  
 A:Gene: NMB0743  
 C:Superfamily: spore germination protein C2; bioC homology

Query Match 77.8%; Score 35; DB 2; Length 245;  
 Best Local Similarity 55.6%; Pred. No. 14;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
 ||| |||||  
 Db 179 FYSFKLLPV 187

RESULT 14  
 JC7359  
 splicing factor, Ssf-1 - human  
 C:Species: Homo sapiens (man)  
 C:Date: 17-Nov-2000 #sequence\_revision 17-Nov-2000 #text\_change 09-Jul-2004  
 C:Accession: JC7359  
 R:Suarez-Huerta, N.; Boeynaems, J.M.; Communi, D.  
 Biochem. Biophys. Res. Commun. 275, 37-42, 2000  
 A:Title: Cloning, genomic organization, and tissue distribution of human Ssf-1.  
 A:Reference number: JC7359  
 A:Accession: JC7359  
 A:Molecule type: mRNA

A:Residues: 1-473 <SUA>  
 A:Cross-references: UNIPROT:Q9NQ55; GB:AJ292529  
 C:Comment: This factor, involved in the second step of mRNA splicing, is a negative regul  
 C:Genetics:  
 A:Gene: Ssf-1  
 A:Map position: 19p31  
 C:Keywords: neutrophil; placenta

Query Match 77.8%; Score 35; DB 2; Length 473;  
 Best Local Similarity 62.5%; Pred. No. 26;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSLKIVPI 9  
 ||| |||||  
 Db 197 YSIKWVPV 204

RESULT 15  
 A40218  
 envelop glycoprotein gp120 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
 C:Accession: A40218  
 R:Turner, S.; Tizard, R.; DeMarinis, J.; Pepinsky, R.B.; Zullo, J.; Schooley, R.; Fisher,  
 Proc. Natl. Acad. Sci. U.S.A. 89, 1335-1339, 1992  
 A:Title: Resistance of primary isolates of human immunodeficiency virus type 1 to neutral  
 A:Reference number: A40218; MUID:92159044; PMID:1741386  
 A:Accession: A40218  
 A:Status: preliminary  
 A:Molecule type: nucleic acid  
 A:Residues: 1-506 <TUR>  
 A:Cross-references: UNIPROT:Q9PY23  
 A:Experimental source: isolate p17  
 A:Note: sequence extracted from NCBI backbone (NCBI:82240)  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: glycoprotein

Query Match 77.8%; Score 35; DB 2; Length 506;  
 Best Local Similarity 77.8%; Pred. No. 28;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
 ||| |||||  
 Db 172 FYKLDIVPI 180

RESULT 16  
 G90593  
 subtilisin, serine proteinase [imported] - Mycoplasma pulmonis (strain UAB CTIP)  
 C:Species: Mycoplasma pulmonis  
 C:Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
 C:Accession: G90593  
 R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;  
 Nucleic Acids Res. 29, 2145-2153, 2001  
 A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm  
 A:Reference number: A99512; MUID:21267165; PMID:11353084  
 A:Accession: G90593  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-553 <KUR>  
 A:Cross-references: UNIPROT:Q98PR4; GB:AL445566; PID:G14090070; PIDN:CAC13828.1; GSPDB:GN  
 A:Experimental source: strain UAB CTIP  
 C:Genetics:  
 A:Gene: MYPV 6550  
 A:Genetic code: SGC3

Query Match 77.8%; Score 35; DB 2; Length 553;  
 Best Local Similarity 77.8%; Pred. No. 31;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
 ||| |||||  
 Db 117 FYSLNIPPI 125

```
RESULT 17
H44001
env polyprotein precursor - human immunodeficiency virus type 1 (strain YU-2)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: H44001
R:Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
J. Virol. 66, 6587-6600, 1992
A:Title: Complete nucleotide sequence, genome organization, and biological properties of
A:Reference number: A44001; MUID:93021387; PMID:1404605
A:Accession: H44001
A:Molecule type: DNA
A:Residues: 1-843 <L1Y>
A:Cross-references: UNIPROT:P35961; GB:M93258
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:19-35/Region: hydrophobic
F:30-489/Product: coat protein gp120 #status predicted <GP1>
F:490-843/Product: coat protein gp41 #status predicted <GP2>
F:499-515/Region: hydrophobic
F:673-689/Region: hydrophobic
F:738-755/Domain: transmembrane #status predicted <TMN>
F:787,129,135,138,154,158,184,193,230,237,258,272,285,291,297,327,351,381,389,395,400,435
Query Match 77.8%; Score 35; DB 1; Length 843;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
DB 174 FVSLDIVPI 182

RESULT 18
VCLJND
env polyprotein precursor - human immunodeficiency virus type 1 (isolate NDK)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: JQ0066
R:Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.;
Gene 81, 275-284, 1989
A:Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human immun
A:Reference number: JQ0065; MUID:90034200; PMID:2806917
A:Accession: JQ0066
A:Molecule type: DNA
A:Residues: 1-846 <SPI>
A:Cross-references: UNIPROT:P18799; GB:M27323; NID:G328154; PIDN:AAA44873.1; PID:G328162
A:Note: the authors translated the codon GCG for residue 523 as Arg
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-501/Product: coat protein gp120 #status predicted <CP1>
F:502-846/Product: coat protein gp41 #status predicted <CP2>
F:502-520/Domain: transmembrane #status predicted <TM1>
F:674-692/Domain: transmembrane #status predicted <TM2>
F:187,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,606
Query Match 77.8%; Score 35; DB 1; Length 846;
Best Local Similarity 77.8%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 FVSLKIVPI 9
DB 167 FYKLDIVPI 175

RESULT 19
VCLJBR
env polyprotein - human immunodeficiency virus type 1 (isolate BR)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C:Accession: A31667
R:Anand, R.; Thayer, R.; Srinivasan, A.; Nayyar, S.; Gardner, M.; Luciw, P.; Dandekar, S.;
Virolgy 168, 79-89, 1989
A:Title: Biological and molecular characterization of human immunodeficiency virus (HIV-1
A:Reference number: A94389; MUID:89085613; PMID:2789516
A:Accession: A31667
A:Molecule type: DNA
A:Residues: 1-852 <ANA>
A:Cross-references: UNIPROT:P12488
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: capsid protein; coat protein; polyprotein; transmembrane protein
F:1-516/Product: coat protein gp120 #status predicted <CP1>
F:517-852/Product: coat protein gp41 #status predicted <CP2>
Query Match 77.8%; Score 35; DB 1; Length 852;
Best Local Similarity 77.8%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
DB 174 FYKLDIVPI 182

RESULT 20
SI3288
env protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: SI3288
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Digne, A.; Idler, K.; Zack, J.A.;
Nature 348, 69-73, 1990
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120 c
A:Reference number: SI3288; MUID:91043044; PMID:2172833
A:Accession: SI3288
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-854 <OBR>
A:Cross-references: UNIPROT:Q85582; UNIPROT:Q72502; UNIPROT:O90178; UNIPROT:Q78243; UNIP
C:Superfamily: type E retrovirus env polyprotein
Query Match 77.8%; Score 35; DB 2; Length 854;
Best Local Similarity 77.8%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
DB 176 FYKLDIVPI 184

RESULT 21
G72754
probable phosphoenolpyruvate synthase APE0028 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: G72754
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
```

A:Reference number: A72450; MUID:99110339; PMID:10382966

A:Accession: G72754

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-218 <KAW>

A:Cross-references: UNIPROT:Q9YGV73; DBJ:AP000058; NID:95103388; PIDN:BAA78937.1; PID:dl

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE0028

Query Match

Best Local Similarity 75.6%; Score 34; DB 2; Length 218;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FYSLKIVP 8

DB 21 FYAMKLVLP 28

RESULT 22

D71805

protein-export membrane protein - Helicobacter pylori (strain J99)

C:Species: Helicobacter pylori

A:Variety: strain J99

C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004

C:Accession: D71805

R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;

Ives, C.; Gibson, R.; Werberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;

Nature 397, 176-180, 1999

A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path

A:Reference number: A71800; MUID:99120557; PMID:9923682

A:Accession: D71805

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-526 <ARN>

A:Cross-references: UNIPROT:Q9ZJ66; GB:AE001567; GB:AE001439; NID:94156065; PIDN:AAD0702

A:Experimental source: strain J99

C:Genetics:

A:Gene: secD

C:Superfamily: protein export membrane protein secD

Query Match

Best Local Similarity 75.6%; Score 34; DB 2; Length 526;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9

DB 122 FYSVKLTPL 130

RESULT 23

A99444

acylaminoacyl-peptidase, probable (apeH-3) [imported] - Sulfolobus solfataricus

C:Species: Sulfolobus solfataricus

C:Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004

C:Accession: A99444

R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-

Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.

arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A:Description: Sulfolobus solfataricus complete genome.

A:Reference number: A99139

A:Accession: A99444

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-591 <KUR>

A:Cross-references: UNIPROT:Q97VD6; GB:AE006641; NID:913816011; PIDN:AAK42808.1; GSPDB:C

C:Genetics:

A:Gene: apeH-3

Query Match

Best Local Similarity 75.6%; Score 34; DB 2; Length 591;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FYSLKIVP 8

DB 7 YYSIKLVP 14

RESULT 24

VCLJKX

env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp32)

N:Alternate names: coat polyprotein

N:Contains: coat protein gp120; coat protein gp32

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 01-Mar-1996

C:Accession: B42995

R:Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.

Virolgy 189, 534-546, 1992

A:Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated t

A:Reference number: A42995; MUID:92351552; PMID:1322587

A:Accession: B42995

A:Molecule type: mRNA

A:Residues: 1-729 <SHI>

A:Cross-references: GB:S41266; GB:D01206

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F:1-689/Domain: extracellular #status predicted <EXT>

F:1-33/Domain: signal sequence #status predicted <SIG>

F:17-33/Region: hydrophobic #status predicted

F:34-517/Product: coat protein gp120 #status predicted <CP1>

F:514-517/Region: cleavage processing #status predicted

F:518-729/Product: coat protein gp32 #status predicted <CP2>

F:518-534/Region: hydrophobic #status predicted

F:690-711/Domain: transmembrane #status predicted <TM1>

F:712-729/Domain: intracellular #status predicted <INT>

F:93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414,

Query Match

Best Local Similarity 75.6%; Score 34; DB 1; Length 729;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9

DB 179 FYKLDVVPI 187

RESULT 25

T09448

envelope glycoprotein - human immunodeficiency virus type 1 (strain JRFL)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

C:Accession: T09448

R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,

submitted to the EMBL Data Library, July 1996

A:Reference number: Z16673

A:Accession: T09448

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-847 <PAN>

A:Cross-references: UNIPROT:Q75760; EMBL:U63632; NID:91465777; PID:91465781

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

Query Match

Best Local Similarity 75.6%; Score 34; DB 2; Length 847;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9

DB 173 FYKLDVVPI 181



```
RESULT 26
S13289
env protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S13289
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
Nature 348, 69-73, 1990
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A:Reference number: S13288; MUID:91043044; PMID:2172833
A:Accession: S13289
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-847 <OR>
A:Cross-references: UNIPROT:Q75760
C:Superfamily: type E retrovirus env polyprotein

Query Match 75.6%; Score 34; DB 2; Length 847;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 173 FYKLDVPI 181

RESULT 27
S33985
env polyprotein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S33985
R:Carlini, F.
submitted to the EMBL Data Library, November 1991
A:Reference number: S33979
A:Accession: S33985
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-851 <CAR>
A:Cross-references: UNIPROT:Q78243; EMBL:Z11530; NID:G60192; PIDN:CAA77628.1; PID:G60199
C:Superfamily: type E retrovirus env polyprotein

Query Match 75.6%; Score 34; DB 2; Length 851;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 176 FYKLDIPI 184

RESULT 28
T12016
envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T12016
R:McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.
AIDS Res. Hum. Retroviruses 14, 329-337, 1998
A:Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in S
A:Reference number: T17379; MUID:98178716; PMID:9519894
A:Accession: T12016
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-852 <MCC>
A:Cross-references: UNIPROT:O41883; EMBL:U90934; NID:G2351783; PIDN:AAC59271.1; PID:G235
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein

Query Match 75.6%; Score 34; DB 2; Length 852;
Best Local Similarity 66.7%; Pred. No. 76;
```

```
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 175 FYKLDVPI 183

RESULT 29
S54384
envelope polyprotein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S54384
R:Theodore, T.; Buckler-White, A.J.
submitted to the EMBL Data Library, July 1989
A:Reference number: S54377
A:Accession: S54384
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-853 <THE>
A:Cross-references: UNIPROT:P12487; EMBL:M22639; NID:G329377; PIDN:AAA45370.1; PID:G32937
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: polyprotein

Query Match 75.6%; Score 34; DB 2; Length 853;
Best Local Similarity 77.8%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 173 FYRLDIVPI 181

RESULT 30
VCLJZR
env polyprotein precursor - human immunodeficiency virus Zr-6
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus Zr-6
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: D26192
R:Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu
Gene 52, 71-82, 1987
A:Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleotic
A:Reference number: A26192; MUID:87248097; PMID:3036660
A:Accession: D26192
A:Molecule type: DNA
A:Residues: 1-855 <SRI>
A:Cross-references: UNIPROT:P04580; GB:K03458; GB:M16322; NID:G329398; PIDN:AAA45380.1; I
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-855/Product: env polyprotein #status predicted <MAT>
F:20-500/Product: exterior membrane glycoprotein #status predicted <EXT>
F:501-855/Product: transmembrane glycoprotein #status predicted <TM>
F:87,129,140,145,154,158,186,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404,

Query Match 75.6%; Score 34; DB 1; Length 855;
Best Local Similarity 77.8%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 174 FYRLDIVPI 182

RESULT 31
A44963
env polyprotein precursor - human immunodeficiency virus type 1 (isolate Z321)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
```

A:Note: host Homo sapiens (man)  
C:Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 09-Jul-2004  
C:Accession: A44963  
R:Srinivasan, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.; McCormick, J.  
AIDS Res. Hum. Retroviruses 5, 121-129, 1989  
A:Title: Molecular characterization of HIV-1 isolated from a serum collected in 1976: nu  
A:Reference number: A44963; MUID:89228766; PMID:2713163  
A:Accession: A44963  
A:Molecule type: DNA  
A:Residues: 1-856 <SRI>  
A:Cross-references: UNIPROT:P05881; GB:M15896; NID:g329394.1; PID:g329394  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-520/Product: coat protein gp120 #status predicted <CP1>  
F:521-856/Product: coat protein gp41 #status predicted <CP2>  
F:864-705/Domain: transmembrane #status predicted <TMN>  
F:87,132,138,152,156,183,198,242,263,277,294,302,339,398,402,411,448,461,462,465,611  
Query Match 75.6%; Score 34; DB 1; Length 856;  
Best Local Similarity 77.8%; Pred. No. 77;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 FYSLKIVPI 9  
DB 172 FYRLDIVPI 180  
RESULT 32  
VCLJ3W  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)  
N:Contains: coat protein gp120; coat protein gp41  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 09-Jul-2004  
C:Accession: A24774  
R:Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.  
Cell 45, 637-648, 1986  
A:Title: Identification and characterization of conserved and variable regions in the en  
A:Reference number: A24774; MUID:86218077; PMID:2423250  
A:Accession: A24774  
A:Molecule type: DNA  
A:Residues: 1-856 <STA>  
A:Cross-references: UNIPROT:P31872; GB:K03455; GB:M38432; NID:g1906382  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-501/Product: coat protein gp120 #status predicted <GP1>  
F:502-847/Product: coat protein gp41 #status predicted <GP2>  
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459  
Query Match 75.6%; Score 34; DB 1; Length 856;  
Best Local Similarity 66.7%; Pred. No. 77;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 FYSLKIVPI 9  
DB 171 FYRLDIVPI 179  
RESULT 33  
VCLJH3  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 09-Jul-2004  
C:Accession: A03973  
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dora  
nberger, J.A.; Papas, T.S.; Ghraryeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.

Nature 313, 277-284, 1985  
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.  
A:Reference number: A93353; MUID:85111123; PMID:2578615  
A:Accession: A03973  
A:Molecule type: DNA  
A:Residues: 1-856 <RAT>  
A:Cross-references: UNIPROT:P03375; GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326;  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:512-856/Product: transmembrane glycoprotein #status predicted <TMN>  
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406,  
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predict  
Query Match 75.6%; Score 34; DB 1; Length 856;  
Best Local Similarity 66.7%; Pred. No. 77;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 FYSLKIVPI 9  
DB 176 FYKLDIPI 184  
RESULT 34  
VCLJVL  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 09-Jul-2004  
C:Accession: A03974  
R:Muscing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Laaky, L.A.; Capon, D.J.  
Nature 313, 450-458, 1985  
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovir  
A:Reference number: A93355; MUID:85111157; PMID:2982104  
A:Accession: A03974  
A:Molecule type: DNA  
A:Residues: 1-856 <MUE>  
A:Cross-references: UNIPROT:P03376; GB:K02083; NID:g555008; PIDN:AAB59873.1; PID:g328559  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:512-856/Product: transmembrane glycoprotein #status predicted <TMN>  
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406,  
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predict  
Query Match 75.6%; Score 34; DB 1; Length 856;  
Best Local Similarity 66.7%; Pred. No. 77;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 FYSLKIVPI 9  
DB 176 FYKLDIPI 184  
RESULT 35  
VCLJSC  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
C:Accession: B28922  
R:Guigo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta  
Virology 164, 531-536, 1988  
A:Title: Envelope sequences of two new United States HIV-1 isolates.  
A:Reference number: A28922; MUID:88219542; PMID:3369091

A:Accession: B28922  
A:Molecule type: DNA  
A:Residues: 1-861 <GUR>  
C:Genetics:  
A:Gene: env

C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane protein  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-861/Product: env polyprotein #status predicted <EPD>  
F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 75.6%; Score 34; DB 1; Length 861;  
Best Local Similarity 66.7%; Pred. No. 77;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9  
|||:|:  
Db 177 FYKLDVPI 185

RESULT 36

VCLJRB env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp41)

N:Alternate names: coat polyprotein  
N:Contains: coat protein gp120; coat protein gp41  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Accession: A42995  
C:Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 09-Jul-2004  
R:Shimizu, H.; Hasebe, F.; Teuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.  
Virolgy 189, 534-546, 1992  
A:Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated  
A:Reference number: A42995; MUID:92351552; PMID:1322587  
A:Accession: A42995  
A:Molecule type: mRNA  
A:Residues: 1-861 <SHI>  
A:Cross-references: UNIPROT:P31819; GB:S41266; GB:D01206

C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
F:1-689/Domain: extracellular #status predicted <EXT>  
F:1-33/Domain: signal sequence #status predicted <SIG>  
F:17-33/Region: hydrophobic #status predicted  
F:134-517/Product: coat protein gp120 #status predicted <CP1>  
F:514-517/Region: cleavage processing #status predicted  
F:518-861/Product: coat protein gp41 #status predicted <CP2>  
F:518-534/Region: hydrophobic #status predicted  
F:690-711/Domain: transmembrane #status predicted <TM1>  
F:712-861/Domain: intracellular #status predicted <INT>  
F:756-772/Region: hydrophobic #status predicted  
F:93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,403,408,414

Query Match 75.6%; Score 34; DB 1; Length 861;  
Best Local Similarity 66.7%; Pred. No. 77;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9  
|||:|:  
Db 179 FYKLDVPI 187

RESULT 37

VCLJLV

env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)

N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 09-Jul-2004  
C:Accession: A03975  
R:Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.  
Cell 40, 9-17, 1985  
A:Title: Nucleotide sequence of the AIDS virus, LAV.

A:Reference number: A90866; MUID:85099333; PMID:2981635

A:Accession: A03975  
A:Molecule type: DNA  
A:Residues: 1-861 <WAL>  
A:Cross-references: UNIPROT:P03377; GB:K02013; NID:g326417; PIDN:AAB59751.1; PID:g326424  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-516/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:517-861/Product: transmembrane glycoprotein #status predicted <TM>  
F:88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411,  
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 75.6%; Score 34; DB 1; Length 861;  
Best Local Similarity 66.7%; Pred. No. 77;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9  
|||:|:  
Db 181 FYKLDIPI 189

RESULT 38

GNVTR

genome polyprotein 2 - tomato ringspot virus (strain raspberry)

N:Contains: coat protein  
C:Species: tomato ringspot virus  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C:Accession: JQ1093  
R:Rott, M.E.; Tremaine, J.H.; Rochon, D.M.  
J. Gen. Virol. 72, 1505-1514, 1991  
A:Title: Nucleotide sequence of tomato ringspot virus RNA-2.  
A:Reference number: JQ1093; MUID:91311402; PMID:1856689  
A:Accession: JQ1093  
A:Molecule type: genomic RNA  
A:Residues: 1-1882 <ROT>  
A:Cross-references: UNIPROT:P25247; GB:D12477; GB:D01129; NID:g222674; PIDN:BA02043.1; I:  
A:Note: it is uncertain whether Met-1 or Met-122 is the initiator  
C:Genetics:

A:Map position: segment 2  
C:Superfamily: tomato ringspot virus genome polyprotein  
C:Keywords: coat protein; glycoprotein; polyprotein  
F:131-1882/Product: coat protein #status predicted <MAT>  
F:269,295,1183,1316,1543,1561,1735/Binding site: carbohydrate (Asn) (covalent) #status p

Query Match 75.6%; Score 34; DB 1; Length 1882;  
Best Local Similarity 55.6%; Pred. No. 1.7e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9  
|||:|:  
Db 806 FYSVKVPI 814

RESULT 39

TI7870

hypothetical protein a370R - Chlorella virus PBCV-1

C:Species: Chlorella virus PBCV-1  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
R:Graves, M.V.; Van Etten, J.L.  
submitted to the EMBL Data Library, May 1999  
A:Reference number: Z18806  
A:Accession: T17870  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-82 <GRA>  
A:Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96738.1  
A:Experimental source: specific host Chlorella strain NC64A  
C:Genetics:  
A:Note: a370R

Query Match 73.3%; Score 33; DB 2; Length 82;  
Best Local Similarity 75.0%; Pred. No. 12;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSLKIVPI 9  
|.:|:|  
Db 60 YALRIVPI 67

RESULT 40  
B87667  
ABC-2 type transporter, probable CC3372 [imported] - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C:Accession: B87667  
R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; MUID:21173698; PMID:11259647  
A:Accession: B87667  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-253 <STO>  
A:Cross-references: UNIPROT:Q9A334; GB:AB005673; NID:gl3425078; PIDN:AAK25334.1; GSPDB:G  
C:Gene: CC3372  
C:Superfamily: Escherichia coli probable ABC transporter yadH

Query Match 73.3%; Score 33; DB 2; Length 253;  
Best Local Similarity 62.5%; Pred. No. 37;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FYSLKIVP 8  
|.:|:|  
Db 185 FYSLKIVP 192

Search completed: February 24, 2005, 19:15:24  
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: February 24, 2005, 18:45:15 ; Search time 174 Seconds  
(without alignments)  
26.487 Million cell updates/sec

Title: US-09-914-205-5  
Perfect score: 45  
Sequence: 1 FYSLKIVPI 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.\*

1: uniprot\_eprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	41	91.1	772	2	Q7F8Q8	Q7F8Q8 oryza sativ
2	40	88.9	260	2	Q8D2S3	Q8D2S3 wigglewort
3	39	86.7	254	2	P88350	P88350 human immun
4	39	86.7	394	2	Q70194	Q70194 human immun
5	39	86.7	460	2	Q9WR10	Q9WR10 human immun
6	39	86.7	494	2	Q71645	Q71645 human immun
7	39	86.7	517	2	Q75603	Q75603 human immun
8	39	86.7	536	2	Q75597	Q75597 human immun
9	39	86.7	540	2	Q75601	Q75601 human immun
10	39	86.7	541	2	Q75599	Q75599 human immun
11	39	86.7	545	2	Q75598	Q75598 human immun
12	39	86.7	843	2	Q6BC09	Q6BC09 human immun
13	39	86.7	846	2	Q6XJ60	Q6XJ60 human immun
14	39	86.7	851	2	Q6HIQ0	Q6HIQ0 human immun
15	39	86.7	864	2	Q92890	Q92890 human immun
16	38	84.4	37	2	Q69722	Q69722 human immun
17	38	84.4	48	2	Q69724	Q69724 human immun
18	38	84.4	52	2	Q69720	Q69720 human immun
19	38	84.4	91	2	Q70903	Q70903 human immun
20	38	84.4	92	2	Q99C16	Q99C16 human immun
21	38	84.4	92	2	Q71257	Q71257 human immun
22	38	84.4	110	2	Q71270	Q71270 human immun
23	38	84.4	215	2	Q8JEC0	Q8JEC0 human immun
24	38	84.4	215	2	Q8Q820	Q8Q820 human immun
25	38	84.4	226	2	Q8Q813	Q8Q813 human immun
26	38	84.4	230	2	Q8Q814	Q8Q814 human immun
27	38	84.4	232	2	Q8Q831	Q8Q831 human immun
28	38	84.4	233	2	Q8JE87	Q8JE87 human immun
29	38	84.4	233	2	Q8JE88	Q8JE88 human immun
30	38	84.4	233	2	Q8Q816	Q8Q816 human immun
31	38	84.4	233	2	Q8Q819	Q8Q819 human immun

32	38	84.4	234	2	Q8Q812	Q8Q812 human immun
33	38	84.4	242	2	Q8JE89	Q8JE89 human immun
34	38	84.4	242	2	Q8Q832	Q8Q832 human immun
35	38	84.4	242	2	Q8Q836	Q8Q836 human immun
36	38	84.4	244	2	P88361	P88361 human immun
37	38	84.4	244	2	Q8Q818	Q8Q818 human immun
38	38	84.4	245	2	Q8Q815	Q8Q815 human immun
39	38	84.4	245	2	Q8Q827	Q8Q827 human immun
40	38	84.4	249	2	P88346	P88346 human immun
41	38	84.4	249	2	P88353	P88353 human immun
42	38	84.4	251	2	P88354	P88354 human immun
43	38	84.4	251	2	P88358	P88358 human immun
44	38	84.4	251	2	Q8Q810	Q8Q810 human immun
45	38	84.4	254	2	P88349	P88349 human immun

ALIGNMENTS

RESULT 1  
Q7F8Q8  
ID Q7F8Q8 PRELIMINARY; PRT; 772 AA.  
AC Q7F8Q8;  
DT 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE Putative leucine-rich repeat transmembrane protein kinase 2.  
GN Name=P0437H03.137;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP000366; BAD15408.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004674; F:protein-tyrosine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR011009; Kinase\_like.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR007090; LRR plant.  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR002290; Ser Thr\_kinase.  
DR InterPro; IPR001245; Tyr\_kinase.  
DR Pfam; PF00560; LRR\_1; 3.  
DR PRINTS; PR000019; LEURICHRPT.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TKc; 1.  
DR SMART; SM00219; TyrKc; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
KW ATP-binding; Kinase; Transmembrane.  
SQ SEQUENCE 772 AA; 84288 MW; 4EAF97FDA1A1C062 CRC64;

Query Match 91.1%; Score 41; DB 2; Length 772;  
Best Local Similarity 77.8%; Pred.No.10;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
| | | | | :  
Db 99 FYSLKILPV 107

RESULT 2  
Q8D2S3  
ID Q8D2S3 PRELIMINARY; PRT; 260 AA.  
AC Q8D2S3;  
DT 01-MAR-2003 (Tremblrel. 23, Created)

```
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Yadh protein.
GN Name=yadh; OrderedLocusNames=WIGBR2810;
OS Wigglesworthia glossinidia brevipalpis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Wigglesworthia.
OX NCBI_TaxID=36870;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22297718; PubMed=12219091; DOI=10.1038/ng986;
RA Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,
RA Aksoy S.;
RT "Genome sequence of the endocellular obligate symbiont of tsetse
RT flies, Wigglesworthia glossinidia."
RL Nat. Genet. 32:402-407(2002).
DR EMBL; AB063521; BAC24427.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000412; ABC 2.
DR Pfam; PF01061; ABC2 membrane; 1.
DR PRINTS; PR00164; ABC2TRNSPORT.
DR PROSITE; PS00890; ABC2_MEMBRANE; 1.
KW Complete proteome.
SQ SEQUENCE 260 AA; 29532 MW; 165F30B1120DCC75 CRC64;

Query Match 88.9%; Score 40; DB 2; Length 260;
Best Local Similarity 77.8%; Pred. No. 5.6;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 192 FYSLKLLPI 200

RESULT 3
P88350
ID P88350 PRELIMINARY; PRT; 254 AA.
AC P88350;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97184515; PubMed=9032317;
RA McDonald R.A., Mayers D.L., Chung R.C., Wagner K.F., Ratto-Kim S.,
RA Birx D.L., Michael N.L.;
RT "Evolution of human immunodeficiency virus type 1 env sequence
RT variation in patients with diverse rates of disease progression and T-
RT cell function."
RL J. Virol. 71:1871-1879(1997).
DR EMBL; U69426; AAC56737.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:00019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 254
FT NON_TER 254
SQ SEQUENCE 254 AA; 28020 MW; B628C9A95F5CB33 CRC64;

Query Match 86.7%; Score 39; DB 2; Length 254;
Best Local Similarity 77.8%; Pred. No. 8.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 FYSLKIVPI 9
Db 64 FYSLNVPI 72

RESULT 4
Q70194
ID Q70194 PRELIMINARY; PRT; 394 AA.
AC Q70194;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94365938; PubMed=8083973;
RA Sabino E.C., Shpaer E.G., Morgado M.G., Korber B.T., Diaz R.S.,
RA Bongertz V., Cavalcante S., Galvao-Castro B., Mullins J.L., Mayer A.;
RT "Identification of human immunodeficiency virus type 1 envelope genes
RT recombinant between subtypes B and F in two epidemiologically linked
RT individuals from Brazil."
RL J. Virol. 68:6340-6346(1994).
DR EMBL; U08974; AAA61531.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 394
FT NON_TER 394
SQ SEQUENCE 394 AA; 43452 MW; 9B1324C0A2D22742 CRC64;

Query Match 86.7%; Score 39; DB 2; Length 394;
Best Local Similarity 88.9%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 55 FYSLDIVPI 63

RESULT 5
Q9WRIO
ID Q9WRIO PRELIMINARY; PRT; 460 AA.
AC Q9WRIO;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=TM013;
RA Blackard J.T., Renjifo B., Klaskala W., Chaplin B.R., Shah P.,
RA McLane M.P., Barin F., Esparza J., Zelaya J.E., Osmanov S., Soto R.,
RA Fernandez J.A., Baum M.K., Essex M.E.;
RT "HIV-1 subtype B in Honduras."
RL Virus Res. 60:191-197(1999).
DR EMBL; AF096688; AAD42104.1; -.
DR HSSP; P19549; IMEQ.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
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DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GPI20.
DR Pfam; PF00516; GPI20; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 460 460
SQ SEQUENCE 460 AA; 51461 MW; FDB9643CA6056C31 CRC64;

Query Match      86.7%; Score 39; DB 2; Length 460;
Best Local Similarity 88.9%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
DB 124 FVSLDIVPI 132

RESULT 6
ID Q71645 PRELIMINARY; PRT; 494 AA.
AC Q71645;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95373135; PubMed=7645211;
RA Arnold C., Balfe P., Clewley J.P.;
RT "Sequence distances between env genes of HIV-1 from individuals
RT infected from the same source: implications for the investigation of
RT possible transmission events.";
RL Virology 211:198-203(1995).
DR EMBL; U23129; AAA80628.1; -.
DR HSP; P04578; IG9W.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0019031; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GPI20.
DR Pfam; PF00516; GPI20; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 494 494
SQ SEQUENCE 494 AA; 55324 MW; BFCC86C039241B8F CRC64;

Query Match      86.7%; Score 39; DB 2; Length 494;
Best Local Similarity 88.9%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
DB 156 FVSLDIVPI 164

RESULT 7
ID Q75603 PRELIMINARY; PRT; 517 AA.
AC Q75603;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein 120 (fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96251941; PubMed=8661395; DOI=10.1006/viro.1996.0332;
RA McKeating J.A., Zhang Y.J., Arnold C., Frederiksson R., Penyo E.M.,
RA Balfe P.;
RT "Chimeric viruses expressing primary envelope glycoproteins of human
RT immunodeficiency virus type I show increased sensitivity to
RT neutralization by human sera.";
RL Virology 220:450-460(1996).
DR EMBL; U57794; AAB17032.1; -.
DR HSP; P19549; 1MEQ.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GPI20.
DR Pfam; PF00516; GPI20; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 517 517
SQ SEQUENCE 517 AA; 27A8C123A434800B CRC64;

Query Match      86.7%; Score 39; DB 2; Length 517;
Best Local Similarity 88.9%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
DB 183 FVSLDIVPI 191

RESULT 8
ID Q75597 PRELIMINARY; PRT; 536 AA.
AC Q75597;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein 120 (fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96251941; PubMed=8661395; DOI=10.1006/viro.1996.0332;
RA McKeating J.A., Zhang Y.J., Arnold C., Frederiksson R., Penyo E.M.,
RA Balfe P.;
RT "Chimeric viruses expressing primary envelope glycoproteins of human
RT immunodeficiency virus type I show increased sensitivity to
RT neutralization by human sera.";
RL Virology 220:450-460(1996).
DR EMBL; U57788; AAB17026.1; -.
DR HSP; P19549; 1MEQ.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GPI20.
DR Pfam; PF00516; GPI20; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 536 536
SQ SEQUENCE 536 AA; 60052 MW; EC1FC0CDB95DB634 CRC64;

Query Match      86.7%; Score 39; DB 2; Length 536;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
DB 179 FVSLDIVPI 187
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RESULT 9
Q75601
ID Q75601 PRELIMINARY; PRT; 540 AA.
AC Q75601;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein 120 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KI4803;
RX MEDLINE=96251941; PubMed=8661395; DOI=10.1006/viro.1996.0332;
RA McKeating J.A., Zhang Y.J., Arnold C., Frederiksson R., Fenyo E.M.,
RA Balfe P.;
RT "Chimeric viruses expressing primary envelope glycoproteins of human
RT immunodeficiency virus type I show increased sensitivity to
RT neutralization by human sera.";
RL Virology 220:450-460(1996).
DR EMBL; U57792; AAB17030.1; -.
DR HSSP; P19549; 1MEQ.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
FT NON_TER 1
FT NON_TER 540
FT NON_TER 540
SQ SEQUENCE 540 AA; 60518 MW; 09BBD63ED3C247F2 CRC64;

Query Match 86.7%; Score 39; DB 2; Length 540;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
Db 180 FVSLDIVPI 188

RESULT 10
Q75599
ID Q75599 PRELIMINARY; PRT; 541 AA.
AC Q75599;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein 120 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KI4803;
RX MEDLINE=96251941; PubMed=8661395; DOI=10.1006/viro.1996.0332;
RA McKeating J.A., Zhang Y.J., Arnold C., Frederiksson R., Fenyo E.M.,
RA Balfe P.;
RT "Chimeric viruses expressing primary envelope glycoproteins of human
RT immunodeficiency virus type I show increased sensitivity to
RT neutralization by human sera.";
RL Virology 220:450-460(1996).
DR EMBL; U57790; AAB17028.1; -.
DR HSSP; P19549; 1MEQ.

Query Match 86.7%; Score 39; DB 2; Length 540;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
Db 180 FVSLDIVPI 188
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DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 541
SQ SEQUENCE 541 AA; 60460 MW; 7514A5AD0ABA6D37 CRC64;

Query Match 86.7%; Score 39; DB 2; Length 541;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
Db 183 FVSLDIVPI 191

RESULT 11
Q75598
ID Q75598 PRELIMINARY; PRT; 545 AA.
AC Q75598;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein 120 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KI4803;
RX MEDLINE=96251941; PubMed=8661395; DOI=10.1006/viro.1996.0332;
RA McKeating J.A., Zhang Y.J., Arnold C., Frederiksson R., Fenyo E.M.,
RA Balfe P.;
RT "Chimeric viruses expressing primary envelope glycoproteins of human
RT immunodeficiency virus type I show increased sensitivity to
RT neutralization by human sera.";
RL Virology 220:450-460(1996).
DR EMBL; U57789; AAB17027.1; -.
DR HSSP; P04578; 1GCI.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
FT NON_TER 1
FT NON_TER 545
FT NON_TER 545
SQ SEQUENCE 545 AA; 60934 MW; 15CD203BB89DEADC CRC64;

Query Match 86.7%; Score 39; DB 2; Length 545;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
Db 185 FVSLDIVPI 193

RESULT 12
Q6BC09
ID Q6BC09 PRELIMINARY; PRT; 843 AA.
AC Q6BC09;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
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DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
 DE Envelope glycoprotein (fragment).  
 GN Name-env;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Binley J.M., Wrin T., Zwick M.B., Korber B., Wang M., Chappey C.,  
 RA Stiegler G., Kunert R., Zolla-Pazner S., Katinger H.,  
 RA Petropoulos C.J., Burton D.R.;  
 RT "Comprehensive analysis of the cross-clade neutralizing activity of a  
 RT panel of anti-Hiv-1 monoclonal antibodies.";  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY669733; AAT67505.1; -;  
 DR GO; GO:0019031; C: viral envelope; IEA.  
 DR GO; GO:0005198; F: structural molecule activity; IEA.  
 DR InterPro; IPR011010; DNA brk\_join\_enz.  
 DR InterPro; IPR000328; Env GP41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 DR Pfam; PF00518; GP120; 1.  
 DR AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
 KW Transmembrane.  
 FT NON TER 843 843  
 SQ SEQUENCE 843 AA; 95773 MW; 4790D380C312969D CRC64;  
  
 Query Match 86.7%; Score 39; DB 2; Length 843;  
 Best Local Similarity 88.9%; Pred. No. 29;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 QY 1 FVSLKIVPI 9  
 DB 168 FVSLDIVPI 176  
  
 RESULT 13  
 Q6XJ60 PRELIMINARY; PRT; 846 AA.  
 AC Q6XJ60;  
 DT 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE Envelope glycoprotein.  
 GN Name-env;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Vachot L., Ataman-Onal Y., Terrat C., Durand P.-Y., Ponceau B.,  
 RA Biron F., Verrier B.;  
 RT "Retrospective Study to Time the Introduction of HIV Type 1 Non-B  
 RT Subtypes in Lyon, France, Using env Genes Obtained from Primary  
 RT Infection Samples.";  
 RL AIDS Res. Hum. Retroviruses 20:687-691 (2004).  
 DR EMBL; AY231157; AAO84281.1; -;  
 DR HSSP; P04578; 1K33.  
 DR GO; GO:0019031; C: viral envelope; IEA.  
 DR GO; GO:0005198; F: structural molecule activity; IEA.  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR000328; Env GP41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 DR PRINTS; PR01415; ANKYRIN  
 DR AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
 KW Transmembrane.  
 SQ SEQUENCE 846 AA; 95186 MW; 726985C4A62FC942 CRC64;  
  
 Query Match 86.7%; Score 39; DB 2; Length 846;  
 Best Local Similarity 88.9%; Pred. No. 29;  
  
 QY 1 FVSLKIVPI 9  
 DB 168 FVSLDIVPI 176  
  
 RESULT 14  
 Q6HIQ0 PRELIMINARY; PRT; 851 AA.  
 AC Q6HIQ0;  
 DT 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE Env glycoprotein.  
 GN Name-env;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Thomson M.M., Sierra M., Tanuri A., Najera R.;  
 RT "Independent origins of human immunodeficiency virus type 1 BF  
 RT intersubtype recombinant viruses from Brazil revealed by analysis of  
 RT near full-length genome sequences.";  
 RL AIDS Res. Hum. Retroviruses 0:0-0 (2004).  
 DR EMBL; AY455782; AAS59219.1; -;  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:0019028; C: viral capsid; IEA.  
 DR GO; GO:0019031; C: viral envelope; IEA.  
 DR GO; GO:0005198; F: structural molecule activity; IEA.  
 DR InterPro; IPR000328; Env GP41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 851 AA; 95766 MW; 92105D4C446660E4 CRC64;  
  
 Query Match 86.7%; Score 39; DB 2; Length 851;  
 Best Local Similarity 88.9%; Pred. No. 29;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 QY 1 FVSLKIVPI 9  
 DB 178 FVSLDIVPI 186  
  
 RESULT 15  
 Q92890 PRELIMINARY; PRT; 864 AA.  
 AC Q92890;  
 DT 01-NOV-1998 (TReMBLrel. 08, Created)  
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE Envelope glycoprotein.  
 GN Name-env;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Celrichs R.B., McPhee D.A., Deacon N.J.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF042102; AAD03215.1; -;  
 DR HSSP; P04578; 1DLB.  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:0019028; C: viral capsid; IEA.  
 DR GO; GO:0019031; C: viral envelope; IEA.  
 DR GO; GO:0005198; F: structural molecule activity; IEA.  
 DR InterPro; IPR000328; Env GP41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.

```
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypeptide; Polypeptide;
KW Transmembrane.
SQ SEQUENCE 864 AA; 97872 MW; E0352117099885E5 CRC64;

Query Match
Best Local Similarity 86.7%; Score 39; DB 2; Length 864;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
Db 182 FVSLDIVPI 190

RESULT 16
Q69722
ID AC Q69722 PRELIMINARY; PRT; 37 AA.
AC Q69722;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein, vlv2 region (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirus; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U09153; AAB53908.1;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
PFam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 37
SQ SEQUENCE 37 AA; 4276 MW; D759287BE6461B99 CRC64;

Query Match
Best Local Similarity 84.4%; Score 38; DB 2; Length 37;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
Db 20 FVSLDIVPI 28

RESULT 17
Q69724
ID AC Q69724 PRELIMINARY; PRT; 48 AA.
AC Q69724;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein, vlv2 region (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirus; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Slobod K.S., Rencher S.D., Farmer A., Smith F.S., Hurwitz J.L.;
RL "HIV type 1 envelope sequence diversity in inner city community.";
RT AIDS Res. Hum. Retroviruses 10:873-875(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U09152; AAB53906.1;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
PFam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 37
SQ SEQUENCE 37 AA; 4276 MW; D759287BE6461B99 CRC64;

Query Match
Best Local Similarity 84.4%; Score 38; DB 2; Length 37;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
Db 20 FVSLDIVPI 28
```

```
RL AIDS Res. Hum. Retroviruses 10:873-875(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U09154; AAB53910.1;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
PFam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 48
SQ SEQUENCE 48 AA; 5535 MW; C9A5381C1523534C CRC64;

Query Match
Best Local Similarity 84.4%; Score 38; DB 2; Length 48;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
Db 28 FVSLDIVPI 36

RESULT 18
Q69720
ID AC Q69720 PRELIMINARY; PRT; 52 AA.
AC Q69720;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein, vlv2 region (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirus; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Slobod K.S., Rencher S.D., Farmer A., Smith F.S., Hurwitz J.L.;
RL "HIV type 1 envelope sequence diversity in inner city community.";
RT AIDS Res. Hum. Retroviruses 10:873-875(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U09152; AAB53906.1;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
PFam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 52
SQ SEQUENCE 52 AA; 5882 MW; 1B12309C68752C73 CRC64;

Query Match
Best Local Similarity 84.4%; Score 38; DB 2; Length 52;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
Db 30 FVSLDIVPI 38

RESULT 19
Q70903
ID AC Q70903 PRELIMINARY; PRT; 91 AA.
RT "HIV type 1 envelope sequence diversity in inner city community.";
```

Qy	1	FYSLKIVPI	9	
Db	58	FYSLDWVPI	66	
RESULT 21				
ID	Q71257	PRELIMINARY;	PRT;	92 AA.
AC	Q71257;			
DT	01-NOV-1996	(T-EMBLrel. 01, Created)		
DT	01-NOV-1996	(T-EMBLrel. 01, Last sequence update)		
DT	01-JUN-2003	(T-EMBLrel. 24, Last annotation update)		
DE	Envelope glycoprotein gp120 (Fragment).			
GN	Name=env;			
OS	Human immunodeficiency virus 1.			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11676;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95191064; PubMed=7884929;			
RA	Wang N., Zhu T., Ho D.D.;			
RT	"Sequence diversity of V1 and V2 domains of gp120 from human			
RT	immunodeficiency virus type 1: lack of correlation with viral			
RT	phenotype.";			
RL	J. Virol. 69:2708-2715(1995).			
DR	EMBL; U19627; AAA68644.1; -.			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0019028; C:viral capsid; IEA.			
DR	GO; GO:0019031; C:viral envelope; IEA.			
DR	GO; GO:0005198; F:structural molecule activity; IEA.			
DR	InterPro; IPR000777; GP120.			
DR	PFam; PF00516; GP120; 1.			
KW	AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.			
FT	NON_TER	1	1	
FT	NON_TER	92	92	
SQ	SEQUENCE 92 AA; 10269 MW; CB58433715CAA880 CRC64;			
Query Match 84.4%; Score 38; DB 2; Length 92;				
Best Local Similarity 77.8%; Pred. No. 5.4;				
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;				
Qy	1	FYSLKIVPI	9	
Db	43	FYSLDWVPI	51	
RESULT 22				
ID	Q71270	PRELIMINARY;	PRT;	110 AA.
AC	Q71270;			
DT	01-NOV-1996	(T-EMBLrel. 01, Created)		
DT	01-NOV-1996	(T-EMBLrel. 01, Last sequence update)		
DT	01-JUN-2003	(T-EMBLrel. 24, Last annotation update)		
DE	Envelope glycoprotein gp120 (Fragment).			
GN	Name=env;			
OS	Human immunodeficiency virus 1.			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11676;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95191064; PubMed=7884929;			
RA	Wang N., Zhu T., Ho D.D.;			
RT	"Sequence diversity of V1 and V2 domains of gp120 from human			
RT	immunodeficiency virus type 1: lack of correlation with viral			
RT	phenotype.";			
RL	J. Virol. 69:2708-2715(1995).			
DR	EMBL; U19640; AAA68657.1; -.			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0019028; C:viral capsid; IEA.			
DR	GO; GO:0019031; C:viral envelope; IEA.			
DR	GO; GO:0005198; F:structural molecule activity; IEA.			
DR	InterPro; IPR000777; GP120.			
DR	PFam; PF00516; GP120; 1.			

KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.  
FT NON\_TER 110  
SQ SEQUENCE 110 AA; 12466 MW; 35D3578DA359196 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 110;  
Best Local Similarity 77.8%; Pred. No. 6.4;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
| | | | : | | |  
Db 62 FYSLDVVPI 70

## RESULT 23

Q8JECO PRELIMINARY; PRT; 215 AA.  
AC Q8JECO;  
DT 01-OCT-2002 (TRENBLrel. 22, Created)  
DT 01-JUN-2002 (TRENBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Takeuchi H., Suzuki Y., Hoshino H., Daar E.S., Koyanagi Y.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB08285; BAC02647.1; -  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.  
FT NON\_TER 215  
SQ SEQUENCE 215 AA; 23687 MW; E08C4B05E07147C8 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 215;  
Best Local Similarity 77.8%; Pred. No. 12;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
| | | | : | | |  
Db 59 FYSLDVVPI 67

## RESULT 24

Q8Q820 PRELIMINARY; PRT; 215 AA.  
AC Q8Q820;  
DT 01-JUN-2002 (TRENBLrel. 21, Created)  
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB077794; BAB85727.1; -  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.  
FT NON\_TER 1  
SQ SEQUENCE 215 AA; 23687 MW; E08C4B05E07147C8 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 215;  
Best Local Similarity 77.8%; Pred. No. 12;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
| | | | : | | |  
Db 59 FYSLDVVPI 67

## RESULT 25

Q8Q813 PRELIMINARY; PRT; 226 AA.  
AC Q8Q813;  
DT 01-JUN-2002 (TRENBLrel. 21, Created)  
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB077801; BAB85734.1; -  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.  
FT NON\_TER 226  
SQ SEQUENCE 226 AA; 25003 MW; 5816FDCFD520D6DA CRC64;

Query Match 84.4%; Score 38; DB 2; Length 226;  
Best Local Similarity 77.8%; Pred. No. 13;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9  
| | | | : | | |  
Db 61 FYSLDVVPI 69

## RESULT 26

Q8Q814 PRELIMINARY; PRT; 230 AA.  
AC Q8Q814;  
DT 01-JUN-2002 (TRENBLrel. 21, Created)  
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB077800; BAB85733.1; -  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.  
FT NON\_TER 230 230  
SQ SEQUENCE 230 AA; 25484 MW; 181C323B143A22D3 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 230;  
Best Local Similarity 77.8%; Pred. No. 13;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9  
|||||:||||  
Db 74 FYSLDVVPI 82

## RESULT 27

ID Q8Q831 PRELIMINARY; PRT; 232 AA.  
AC Q8Q831;  
DT 01-JUN-2002 (TRENBLrel. 21, Created)  
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB077782; BAB85716.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.  
FT NON\_TER 232 232  
SQ SEQUENCE 232 AA; 25529 MW; CC6AD5DD7964104B CRC64;

Query Match 84.4%; Score 38; DB 2; Length 232;  
Best Local Similarity 77.8%; Pred. No. 13;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9  
|||||:||||  
Db 76 FYSLDVVPI 84

## RESULT 28

ID Q8JE87 PRELIMINARY; PRT; 233 AA.  
AC Q8JE87;  
DT 01-OCT-2002 (TRENBLrel. 22, Created)  
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Takeuchi H., Suzuki Y., Hoshino H., Daar E.S., Koyanagi Y.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB086318; BAC02680.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.  
FT NON\_TER 233 233  
SQ SEQUENCE 233 AA; 25810 MW; F101792FD2515941 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 233;  
Best Local Similarity 77.8%; Pred. No. 13;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9  
|||||:||||  
Db 61 FYSLDVVPI 69

## RESULT 29

ID Q8JE88 PRELIMINARY; PRT; 233 AA.  
AC Q8JE88;  
DT 01-OCT-2002 (TRENBLrel. 22, Created)  
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Takeuchi H., Suzuki Y., Hoshino H., Daar E.S., Koyanagi Y.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB086317; BAC02679.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR008985; ConA\_like\_lec\_gl.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.  
FT NON\_TER 233 233  
SQ SEQUENCE 233 AA; 25680 MW; E07FDEF7B83C3A21 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 233;  
Best Local Similarity 77.8%; Pred. No. 13;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9  
|||||:||||  
Db 76 FYSLDVVPI 84

## RESULT 30

ID Q8Q816 PRELIMINARY; PRT; 233 AA.  
AC Q8Q816;  
DT 01-JUN-2002 (TRENBLrel. 21, Created)  
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB077798; BAB85731.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.  
 FT NON\_TER 233 233  
 SQ SEQUENCE 233 AA; 25810 MW; F101792FD2515941 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 233;  
 Best Local Similarity 77.8%; Pred. No. 13;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9  
 ||||:||||  
 Db 61 FYSLDVVPI 69

## RESULT 31

Q8Q819 PRELIMINARY; PRT; 233 AA.  
 AC Q8Q819;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DE Envelope glycoprotein (Fragment).  
 GN Name=env;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB077795; BAB85728.1; --  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR008985; ConA\_like\_lec\_gl.  
 DR InterPro; IPR00777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.  
 FT NON\_TER 233 233  
 SQ SEQUENCE 233 AA; 25680 MW; E07FDEF7B83C3A21 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 233;  
 Best Local Similarity 77.8%; Pred. No. 13;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9  
 ||||:||||  
 Db 76 FYSLDVVPI 84

## RESULT 32

Q8Q812 PRELIMINARY; PRT; 234 AA.  
 AC Q8Q812;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DE Envelope glycoprotein (Fragment).  
 GN Name=env;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AB077802; BAB85735.1; --  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.  
 FT NON\_TER 234 234  
 SQ SEQUENCE 234 AA; 25944 MW; 096B484F44880D8D CRC64;

Query Match 84.4%; Score 38; DB 2; Length 234;  
 Best Local Similarity 77.8%; Pred. No. 13;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9  
 ||||:||||  
 Db 61 FYSLDVVPI 69

## RESULT 33

Q8JE89 PRELIMINARY; PRT; 242 AA.  
 AC Q8JE89;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DE Envelope glycoprotein (Fragment).  
 GN Name=env;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Takeuchi H., Suzuki Y., Hoshino H., Daar E.S., Koyanagi Y.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB086316; BAC02678.1; --  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.  
 FT NON\_TER 242 242  
 SQ SEQUENCE 242 AA; 26715 MW; 1C0C2D1685D5380 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 242;  
 Best Local Similarity 77.8%; Pred. No. 14;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9  
 ||||:||||  
 Db 86 FYSLDVVPI 94

## RESULT 34

Q8Q832 PRELIMINARY; PRT; 242 AA.  
 AC Q8Q832;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DE Envelope glycoprotein (Fragment).  
 GN Name=env;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB077781; BAB85715.1; -.  
DR GO; GO:0016021; C: integral to membrane; IEA.  
DR GO; GO:0019028; C: viral capsid; IEA.  
DR GO; GO:0019031; C: viral envelope; IEA.  
DR GO; GO:0005198; F: structural molecule activity; IEA.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.  
FT NON\_TER 242 242  
SQ SEQUENCE 242 AA; 26715 MW; 1C0C2D1685505380 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 242;  
Best Local Similarity 77.8%; Pred. No. 14;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9  
Db 86 FYSLDVVPI 94  
|||||:||||

RESULT 35  
Q8Q836 PRELIMINARY; PRT; 242 AA.  
ID Q8Q836  
AC Q8Q836  
DT 01-JUN-2002 (TRENBLrel. 21, Created)  
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB077777; BAB85711.1; -.  
DR GO; GO:0016021; C: integral to membrane; IEA.  
DR GO; GO:0019028; C: viral capsid; IEA.  
DR GO; GO:0019031; C: viral envelope; IEA.  
DR GO; GO:0005198; F: structural molecule activity; IEA.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.  
FT NON\_TER 242 242  
SQ SEQUENCE 242 AA; 26613 MW; 4D616E967D6786CD CRC64;

Query Match 84.4%; Score 38; DB 2; Length 242;  
Best Local Similarity 77.8%; Pred. No. 14;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9  
Db 86 FYSLDVVPI 94  
|||||:||||

RESULT 36  
P88361 PRELIMINARY; PRT; 244 AA.  
ID P88361  
AC P88361  
DT 01-MAY-1997 (TRENBLrel. 03, Created)  
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.

RA MEDLINE=97184515; PubMed=9032317;  
RA McDonald R.A., Mayers D.L., Chung R.C., Wagner K.F., Ratto-Kim S.,  
RA Bix D.L., Michael N.L.;  
RT "Evolution of human immunodeficiency virus type 1 env sequence  
RT variation in patients with diverse rates of disease progression and T-  
RT cell function.";  
RL J. Virol. 71:1871-1879(1997).  
DR EMBL; U69437; AAC56748.1; -.  
DR GO; GO:0016021; C: integral to membrane; IEA.  
DR GO; GO:0019028; C: viral capsid; IEA.  
DR GO; GO:0019031; C: viral envelope; IEA.  
DR GO; GO:0005198; F: structural molecule activity; IEA.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.  
FT NON\_TER 244 244  
SQ SEQUENCE 244 AA; 27027 MW; 37164D083DDAC3D1 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 244;  
Best Local Similarity 77.8%; Pred. No. 14;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9  
Db 58 FYSLDVVPI 66  
|||||:||||

RESULT 37  
Q8Q818 PRELIMINARY; PRT; 244 AA.  
ID Q8Q818  
AC Q8Q818  
DT 01-JUN-2002 (TRENBLrel. 21, Created)  
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB077796; BAB85729.1; -.  
DR GO; GO:0016021; C: integral to membrane; IEA.  
DR GO; GO:0019028; C: viral capsid; IEA.  
DR GO; GO:0019031; C: viral envelope; IEA.  
DR GO; GO:0005198; F: structural molecule activity; IEA.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.  
FT NON\_TER 244 244  
SQ SEQUENCE 244 AA; 27115 MW; 6855D05984F1EBDA CRC64;

Query Match 84.4%; Score 38; DB 2; Length 244;  
Best Local Similarity 77.8%; Pred. No. 14;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9  
Db 61 FYSLDVVPI 69  
|||||:||||

RESULT 38  
Q8Q815 PRELIMINARY; PRT; 245 AA.  
ID Q8Q815  
AC Q8Q815  
DT 01-JUN-2002 (TRENBLrel. 21, Created)  
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).

```
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB077799; BAB85732.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 245
SQ SEQUENCE 245 AA; 27285 MW; 6B11726B82AA3EE5 CRC64;

Query Match      84.4%; Score 38; DB 2; Length 245;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
DB 64 FYSLDVVPI 72

RESULT 39
Q80827 PRELIMINARY; PRT; 248 AA.
AC Q80827;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB077786; BAB85720.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 248
SQ SEQUENCE 248 AA; 27443 MW; 98CB3F4051C823D4 CRC64;

Query Match      84.4%; Score 38; DB 2; Length 248;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
DB 85 FYSLDVVPI 93

RESULT 40
P88346 PRELIMINARY; PRT; 249 AA.
AC P88346;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
```

```
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA McDonald R.A., Mayers D.L., Chung R.C., Wagner K.F., Ratto-Kim S.,
RA Birk D.L., Michael N.L.;
RT "Evolution of human immunodeficiency virus type 1 env sequence
RT variation in patients with diverse rates of disease progression and T-
RT cell function.";
RL J. Virol. 71:1871-1879(1997).
DR EMBL; U69422; AAC56733.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 249
SQ SEQUENCE 249 AA; 27639 MW; B3975A61EE9E2DD0 CRC64;

Query Match      84.4%; Score 38; DB 2; Length 249;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
DB 62 FYSLDVVPI 70
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Search completed: February 24, 2005, 19:14:38  
Job time : 176 secs